

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: June 6, 2004, 10:01:11 ; Search time 2267 Seconds  
(without alignments)  
5965.164 Million cell updates/sec

Title: US-10-081-817A-3

Perfect score: 312

Sequence: 1 atgaagctgcgcgcctcct.....gggcccctgacagtgttggc 312

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl.\*

1: gb.ba.\*

2: gb.htg.\*

3: gb.in.\*

4: gb.cm.\*

5: gb.ov.\*

6: gb.pat.\*

7: gb.ph.\*

8: gb.pl.\*

9: gb.pr.\*

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17: em.hum.\*

18: em.in.\*

19: em.mu.\*

20: em.om.\*

21: em.or.\*

22: em.ov.\*

23: em.pat.\*

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40: em.htgo.mus.\*

41: em.htgo.other.\*

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

# SUMMARIES

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3	308.8	99.0	471	9	HUMZB52D10	AF086152 Homo sapi
4	308.8	99.0	503	9	BC029176	BC029176 Homo sapi
5	308.8	99.0	519	6	BD082142	BD082142 Reagents
6	308.8	99.0	543	6	BD222719	BD222719 Human sig
7	308.8	99.0	543	6	BD226775	BD226775 A novel m
8	308.8	99.0	562	6	BD082141	BD082141 Reagents
9	308.8	99.0	569	6	AX201348	AX201348 Sequence
10	308.8	99.0	570	6	AR252648	AR252648 Sequence
11	308.8	99.0	570	6	AX403520	AX403520 Sequence
12	308.8	99.0	570	9	AY359064	AY359064 Homo sapi
13	307.2	98.5	347	9	AF313458	AF313458 Homo sapi
14	238.2	76.3	130129	2	AC108083	AC108083 Homo sapi
15	238.2	76.3	166777	2	AC106813	AC106813 Homo sapi
16	238.2	76.3	168347	2	AC025336	AC025336 Homo sapi
17	238.2	76.3	190024	9	AC122714	AC122714 Homo sapi
18	227.2	72.8	127488	2	AC022095	AC022095 Homo sapi
19	183	58.7	225	6	BD082139	BD082139 Reagents
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21	162.8	52.2	244	6	BD082138	BD082138 Reagents
22	108.2	34.7	377	10	AF436840	AF436840 Mus muscu
23	108.2	34.7	525	10	AF313456	AF313456 Mus muscu
24	106.6	34.2	331	10	AF436841	AF436841 Rattus no
25	90.4	29.0	245659	2	AC098957	AC098957 Rattus no
26	90.4	29.0	283593	2	AC131433	AC131433 Rattus no
27	90	28.8	630	10	AF313457	AF313457 Mus muscu
28	88.4	28.3	25981	10	AL606479	AL606479 Mouse DNA
29	65.8	21.1	190	6	BD082137	BD082137 Reagents
30	56.4	18.1	366	9	AF313455	AF313455 Homo sapi
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32	56.4	18.1	507	9	AF439545	AF439545 Homo sapi
33	56.4	18.1	508	6	AX376176	AX376176 Sequence
34	56.4	18.1	508	9	AY358979	AY358979 Homo sapi
35	56.4	18.1	531	6	BD222720	BD222720 Human sig
36	56.4	18.1	550	9	BC024232	BC024232 Homo sapi
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44	52.8	16.9	853	10	AF274961	AF274961 Mus muscu
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# ALIGNMENTS

RESULT 1  
AY040564  
LOCUS  
DEFINITION Homo sapiens HIN-1 putative cytokine mRNA, complete cds.  
ACCESSION AY040564  
VERSION AY040564.1 GI:15079187  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM  
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE  
1 (bases 1 to 461)  
Krop, I.E., Sgroi, D., Porter, D.A., Lunetta, K.L., LeVangie, R.,  
Seth, P., Kaelin, C.M., Rhelin, D., Razumovic, J. and Polyak, K.  
Marks, J.R., Pagon, Z., Belina, D., Razumovic, J. and Polyak, K.

Pred. No. is the number of results predicted by chance to have a



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REFERENCE 2 (bases 1 to 471)
AUTHORS Waterston,R.
TITLE Direct Submission
JOURNAL Submitted (24-AUG-1998) Department of Genetics, Washington
University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
COMMENT SUBMITTED BY:
Genome Sequencing Center
Department of Genetics
Washington University
St. Louis MO 63108, USA
http://genome.wustl.edu/gsc
mailto:estewartson.wustl.edu

NOTICE: This sequence represents the full insert of this cDNA. No
attempt has been made to verify whether this corresponds to the
full-length of the original mRNA from which it was derived. We
have tried to obtain double-stranded, or double chemistry sequence
across the entire clone, but potentially, there are areas in the
sequence where this level of coverage was not achieved.
Nevertheless, we are confident of the accuracy of this sequence as
all regions of low quality, as defined by PHRAP (P. Green, in
preparation), were visually inspected and edited accordingly. The
consensus quality values for this sequence have been submitted
separately.

The location of this clone is unknown.
FEATURES             source
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                /clone="IMAGE:307219"
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Best Local Similarity 99.4%; Pred. No. 6e-39;
Matches 310; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 ATGAGCTGCGCGCCCTGCTGGGCTCTGGTGGCCCTGCTGCTGAGCTCCGCTCGT 60
Db 22 ATGAGCTGCGCGCCCTGCTGGGCTCTGGTGGCCCTGCTGCTGAGCTCCGCTCGT 81
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QY 121 GAGCGCGCGCGCGGACCTTGGCCACCCCTCGGCACCTCAACCCGCTGAAGCTCCTG 180
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QY 181 CTGAGCAGCTGGGATCCCGTGAACACCTCATAGAGGGCTCCAGAGTGTGGCT 240
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Db 262 GAGCTGGGTCCCGAGCGCGTGGGGCGCGTGAAGCCCTGAAGCCCTGCTGGGGCGCCTG 321
QY 301 ACAGTGTGGC 312
Db 322 ACAGTGTGGC 333

RESULT 4
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LOCUS Homo sapiens secretoglobin, family 3A, member 1, mRNA PRI 07-OCT-2003
DEFINITION MGC:34758 IMAGE:5180304, complete cds.
ACCESSION BC029176
VERSION BC029176.1 GI:20809672
KEYWORDS MGC.
SOURCE Homo sapiens (human)

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## ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 503)

Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D., Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K., Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F., Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L., Stapleton,M., Soares,M.B., Bonaldo,M.P., Casavant,T.L., Scheetz,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S., Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J., Abramson,R.D., Mullany,S.J., Bosak,S.A., McEwan,P.J., McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S., Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W., Villalón,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A., Fahy,J., Helton,E., Kettman,M., Madan,A., Rodriguez,S., Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y., Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D., Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M., Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smallos,D.E., Scherch,A., Schein,J.E., Jones,S.J. and Marra,M.A.

Generation and initial analysis of more than 15,000 full-length

human and mouse cDNA sequences

Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)

22388257

12477932

2 (bases 1 to 503)

Strausberg,R.

Direct Submission

Submitted (01-MAY-2002) National Institutes of Health, Mammalian

Gene Collection (MGC), Cancer Genomics Office, National Cancer

Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,

USA

NIH-MGC Project URL: <http://mgc.nci.nih.gov>

Contact: MGC help desk

Email: [cgapbs-remail.nih.gov](mailto:cgapbs-remail.nih.gov)

Tissue Procurement: Life Technologies, Inc.

cDNA Library Preparation: Life Technologies, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Baylor College of Medicine Human Genome

Sequencing Center

Center code: BCM-HGSC

Web site: <http://www.hgsc.bcm.tmc.edu/cdna/>Contact: [angbcm.tmc.edu](mailto:angbcm.tmc.edu)

Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Loulseged, H.,

Kowis, C.R., Sneed, A.J., Martin, R.G., Muzny, D.M., Nanavati,

A.N., Gibbs, R.A.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>

Series: IRAP Plate: 50 Row: b Column: 24.

Location/Qualifiers

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/tissue\_type="Brain, Lung, Testis, adult, pooled whole"

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/lab\_host="DH103"

/note="Vector: pCMV-SPORT6"

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Query Match 99.0%; Score 308.8; DB 9; Length 503;  
Best Local Similarity 99.4%; Pred. No. 5.9e-39;  
Matches 310; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 1 ATGAAGCTCGCGGCTCTCTGGGCTCTGCTGGCCCTGCTCTGAGCTCGCTCGTCTGCT 60  
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QY 61 TTCTTAGTGGCTCGGCAAGCTCTGCTGGCCAGCTCTGCTGGCTGGAGTTCGGCGCG 120  
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DB 316 ACAGTGTGTTGGC 327

RESULT 5  
BD082142  
LOCUS  
DEFINITION Reagents and methods useful for detecting diseases of the lung.  
ACCESSION BD082142  
VERSION BD082142.1 GI:22627752  
KEYWORDS JP 2001522225-A/6.  
SOURCE Zea mays  
ORGANISM Zea mays  
REFERENCE 1 (bases 1 to 519)  
AUTHORS Medel,P.A.B., Cohen,M., Colpitts,T.L., Friedman,P.N., Gordon,J., Granados,E.N., Hodges,S.C., Klass,M.R., Kratochvil,J.D., Rapp,L.R., Russell,J.C. and Stroupe,S.D.  
TITLE Reagents and methods useful for detecting diseases of the lung  
JOURNAL Patent: JP 2001522225-A 6 13-NOV-2001;  
COMMENT ABBOTT LABORATORIES  
PD JP 2001522225-A/6  
PF 13-NOV-2001  
PI 30-JAN-1998 JP 1998533078  
PI 31-JAN-1997 US 08/791710  
PI PATRICIA A BILLING MEDEL,MAURICE COHEN,TRACEY L COLPITTS,PAULA N FRIEDMAN,  
PI JULIAN GORDON,EDWARD N GRANADOS,STEVEN C HODGES,MICHAEL R PI  
PI JON D KRATOCHVIL,LISA ROBERTS RAPP,JOHN C RUSSELL,STEPHEN D  
PI STROUPE  
PC C12N15/63,C12N5/10,C12Q1/68,C07K16/47//C07K16/30,G01N33/574 CC  
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Topology: Linear;  
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Best Local Similarity 99.4%; Pred. No. 5.8e-39;  
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DB 379 ACAGTGTGTTGGC 390

RESULT 6  
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LOCUS  
DEFINITION Human signal peptide-containing protein.  
ACCESSION BD222719  
VERSION BD222719.1 GI:33032489  
KEYWORDS JP 2002519030-A/65.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
REFERENCE 1 (bases 1 to 543)  
AUTHORS Lal,P., Tang,Y.T., Gorgone,G.A., Corley,N.C., Guegler,K.J., Baughm,M.R., Akerblom,I.E., Young,J.A., Yue,H., Patterson,C., Reddy,R., Hillman,J.L. and Bandman,O.  
TITLE Human signal peptide-containing protein  
JOURNAL Patent: JP 2002519030-A 65 02-JUL-2002;  
COMMENT INCYTE PHARMACEUTICALS INC  
OS Homo sapiens (human)  
PD JP 2002519030-A/65  
PF 02-JUL-2002  
PI 25-JUN-1999 JP 2000557363  
PI 26-JUN-1998 US 60/090762,31-JUL-1998 US 60/094983 PR  
01-OCT-1998 US 60/102686,11-DEC-1998 US 60/113129 PI PREETI  
LAL,Y TOM TANG,GINA A GORGONE,NEIL C CORLEY,KARL J PI GUEGLER,  
PI MARIAN R BAUGHN,INGRID E AKERBLUM,JANICE AU YOUNG,HENRY YUE,  
PI CHANDRA PATERSON,ROOPA REDDY,JENNIFER L HILLMAN,OLGA BANDMAN  
PC C12N15/09,A61K38/00,A61K39/395,A61K45/00,A61P9/00,A61P15/00,  
PC A61E25/00,  
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C12N15/00,  
PC A61K37/02 C12N5/00  
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FH Key Location/Qualifiers  
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QY 301 ACAGTGTGGC 312
Db 422 ACAGTGTGGC 433

RESULT 9
LOCUS AX201348 569 bp DNA linear PAT 30-AUG-2001
DEFINITION Sequence 27 from Patent WO0153486.
ACCESSION AX201348
VERSION AX201348.1 GI:15391167
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Hillan,K.J., Goddard,A., Godowski,P.J., Gurney,A.L.,
Stone,D.M., Watanabe,C.K., Pan,J., Pitti,R.M., Roy,M.A., Smith,V.,
Compositions and Methods for the treatment of tumour
JOURNAL Patent: WO 0153486-A 27 26-JUL-2001;
Genentech, Inc. (US)
FEATURES
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/db_xref="taxon:9606"
ORIGIN
Query Match 99.0%; Score 308.8; DB 6; Length 569;
Best Local Similarity 99.4%; Pred. No. 5.7e-39;
Matches 310; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 ATGAAGCTCGCGCCCTCTGGGGCTCTGCTGGCCCTGTGCTGAGCTCGCTCGTGTGCT 60
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Db 379 ACAGTGTGGC 390

RESULT 11
LOCUS AX403520 570 bp DNA linear PAT 14-JUN-2002
DEFINITION Sequence 407 from Patent WO0073454.
ACCESSION AX403520
VERSION AX403520.1 GI:21437002
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Ashkenazi,A.J., Baker,K.P., Botstein,D., Desnoyers,L., Eaton,D.,
Ferrara,N., Gerber,H., Gerritsen,M., Goddard,A., Godowski,P.,
Grimaldi,C.O., Gurney,A.B., Kljavin,I., Napier,M.A., Pan,J.,
Paoni,N.F., Roy,M., Stewart,T.A., Tumas,D., Watanabe,C.K.,
Williams,P., Wood,W.I. and Zhang,Z.
Secreted and transmembrane polypeptides and nucleic acids encoding
the same
JOURNAL Patent: WO 0073454-A 407 07-DEC-2000;
Genentech Inc. (US)
FEATURES
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ORIGIN
Query Match 99.0%; Score 308.8; DB 6; Length 570;
Best Local Similarity 99.4%; Pred. No. 5.7e-39;
Matches 310; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 ATGAAGCTCGCGCCCTCTGGGGCTCTGCTGGCCCTGTGCTGAGCTCGCTCGTGTGCT 60
Db 79 ATGAGCTCGCGCCCTCTGGGGCTCTGCTGGCCCTGTGCTGAGCTCGCTCGTGTGCT 138
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Db 259 CTGAGCAGCTGGGCAATCCCGCTGAACCACTCATAGAGGCTCCCAAGAGTGTGTGGCT 318
QY 241 GAGCTGGTCCCAAGGCGGTGGGGCCGTGAAGCCCTGAAGGCCCTGCTGGGGCCCTG 300
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QY 301 ACAGTGTGGC 312
Db 379 ACAGTGTGGC 390
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RESULT 10
LOCUS AR252648 570 bp DNA linear PAT 20-DEC-2002
DEFINITION Sequence 407 from patent US 6479825.
ACCESSION AR252648
VERSION AR252648.1 GI:27300556
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 570)
AUTHORS Winterbottom,J.M., Shimp,L., Boyce,T.M. and Kaes,D.
TITLE Implant, method of making same and use of the implant for the
treatment of bone defects
JOURNAL Patent: US 6479825-A 407 12-NOV-2002;
Genentech Inc. (US)
FEATURES
source
1..570
/mol_type="genomic DNA"
ORIGIN
Query Match 99.0%; Score 308.8; DB 6; Length 570;
Best Local Similarity 99.4%; Pred. No. 5.7e-39;
Matches 310; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 ATGAAGCTCGCGCCCTCTGGGGCTCTGCTGGCCCTGTGCTGAGCTCGCTCGTGTGCT 60
Db 79 ATGAGCTCGCGCCCTCTGGGGCTCTGCTGGCCCTGTGCTGAGCTCGCTCGTGTGCT 138
QY 61 TTCTTAGTGGCTCGGCAAGCTGTGGCCAGCTGTGGCCAGCTGTGCTGAGTGGCGGCG 120
Db 139 TTCTTAGTGGCTCGGCAAGCTGTGGCCAGCTGTGGCCAGCTGTGCTGAGTGGCGGCG 198
QY 121 GAGCCGGGCGGGACCTGGCCCAACCCCTCGGACCCCTCAACCCGCTGAAGCTCCTG 180
Db 199 GAGCCGGGCGGGACCTGGCCCAACCCCTCGGACCCCTCAACCCGCTGAAGCTCCTG 258
QY 181 CTGAGCAGCTGGGCAATCCCGCTGAACCACTCATAGAGGCTCCCAAGAGTGTGTGGCT 240
Db 259 CTGAGCAGCTGGGCAATCCCGCTGAACCACTCATAGAGGCTCCCAAGAGTGTGTGGCT 318
QY 241 GAGCTGGTCCCAAGGCGGTGGGGCCGTGAAGCCCTGAAGGCCCTGCTGGGGCCCTG 300
Db 319 GAGCTGGTCCCAAGGCGGTGGGGCCGTGAAGCCCTGAAGGCCCTGCTGGGGCCCTG 378
QY 301 ACAGTGTGGC 312
Db 379 ACAGTGTGGC 390

RESULT 11
LOCUS AX403520 570 bp DNA linear PAT 14-JUN-2002
DEFINITION Sequence 407 from Patent WO0073454.
ACCESSION AX403520
VERSION AX403520.1 GI:21437002
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Ashkenazi,A.J., Baker,K.P., Botstein,D., Desnoyers,L., Eaton,D.,
Ferrara,N., Gerber,H., Gerritsen,M., Goddard,A., Godowski,P.,
Grimaldi,C.O., Gurney,A.B., Kljavin,I., Napier,M.A., Pan,J.,
Paoni,N.F., Roy,M., Stewart,T.A., Tumas,D., Watanabe,C.K.,
Williams,P., Wood,W.I. and Zhang,Z.
Secreted and transmembrane polypeptides and nucleic acids encoding
the same
JOURNAL Patent: WO 0073454-A 407 07-DEC-2000;
Genentech Inc. (US)
FEATURES
source
1..570
/mol_type="genomic DNA"
ORIGIN
Query Match 99.0%; Score 308.8; DB 6; Length 570;
Best Local Similarity 99.4%; Pred. No. 5.7e-39;
Matches 310; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 ATGAAGCTCGCGCCCTCTGGGGCTCTGCTGGCCCTGTGCTGAGCTCGCTCGTGTGCT 60
Db 79 ATGAGCTCGCGCCCTCTGGGGCTCTGCTGGCCCTGTGCTGAGCTCGCTCGTGTGCT 138
QY 61 TTCTTAGTGGCTCGGCAAGCTGTGGCCAGCTGTGGCCAGCTGTGCTGAGTGGCGGCG 120
Db 139 TTCTTAGTGGCTCGGCAAGCTGTGGCCAGCTGTGGCCAGCTGTGCTGAGTGGCGGCG 198
QY 121 GAGCCGGGCGGGACCTGGCCCAACCCCTCGGACCCCTCAACCCGCTGAAGCTCCTG 180
Db 199 GAGCCGGGCGGGACCTGGCCCAACCCCTCGGACCCCTCAACCCGCTGAAGCTCCTG 258
QY 181 CTGAGCAGCTGGGCAATCCCGCTGAACCACTCATAGAGGCTCCCAAGAGTGTGTGGCT 240
Db 259 CTGAGCAGCTGGGCAATCCCGCTGAACCACTCATAGAGGCTCCCAAGAGTGTGTGGCT 318
QY 241 GAGCTGGTCCCAAGGCGGTGGGGCCGTGAAGCCCTGAAGGCCCTGCTGGGGCCCTG 300
Db 319 GAGCTGGTCCCAAGGCGGTGGGGCCGTGAAGCCCTGAAGGCCCTGCTGGGGCCCTG 378
QY 301 ACAGTGTGGC 312
Db 379 ACAGTGTGGC 390
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/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

ORIGIN
Query Match 99.0%; Score 308.8; DB 6; Length 570;
Best Local Similarity 99.4%; Pred. No. 5.7e-39;
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1 ATGAAGCTCGCGCGCTCTCTGGGGCTCTGCGTGGCGCTCTGCTGAGCTCGCTGCTGCT 60
79 ATGAAGCTCGCGCGCTCTCTGGGGCTCTGCGTGGCGCTCTGCTGAGCTCGCTGCTGCT 138
61 TTCTTAGTGGCTCGCGCAAGCTCTGCGCCAGCTCTGCTGCGCTGCTGAGTGGCGGCG 120
139 TTCTTAGTGGCTCGCGCAAGCTCTGCGCCAGCTCTGCTGCGCTGCTGAGTGGCGGCG 198
121 GAGCGCGCGCGCGCAAGCTCTGCGCCAGCTCTGCGCCAGCTCTGCGCCAGCTCTGCTG 180
199 GAGCGCGCGCGCGCAAGCTCTGCGCCAGCTCTGCGCCAGCTCTGCGCCAGCTCTGCTG 258
181 CTGAGCAGCTCGCGCATCCCTGCAACCTCTGAGGGCTCTGAGGGCTCTGAGGGCTCTG 240
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301 ACAGTGTGTTGGC 312
379 ACAGTGTGTTGGC 390

RESULT 12
AY359064
LOCUS Homo sapiens clone DNA64884 SCGB3A1 (UNQ629) mRNA, complete cds.
DEFINITION AY359064.1 GI:37183245
ACCESSION AY359064.1
VERSION AY359064.1
KEYWORDS Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 570)
AUTHORS Clark,H.F., Gurney,A.L., Abaya,E., Baker,K., Baldwin,D., Brush,J.,
Chen,J., Chow,B., Chui,C., Crowley,C., Currell,B., Deuel,B.,
Dowd,P., Eaton,D., Foster,J., Grimaldi,C., Gu,Q., Hass,P.E.,
Heldens,S., Huang,A., Kim,H.S., Klimowski,L., Jin,Y., Johnson,S.,
Lee,J., Lewis,L., Liao,D., Mark,M., Robbie,E., Sanchez,C.,
Schoenfeld,J., Seshagiri,S., Simmons,J., Singh,J., Smith,V.,
Stinson,J., Vagts,A., Vanden,R., Watanabe,C., Wiedand,B., Woods,K.,
Xie,M.H., Yansura,D., Yi,S., Yu,G., Yuan,J., Zhang,M., Zhang,Z.,
Goddard,A., Wood,W.I. and Godowski,P.
The Secreted Protein Discovery Initiative (SPDI), a Large-Scale
Effort to Identify Novel Human Secreted and Transmembrane Proteins:
A Bioinformatics Assessment
Genome Res. 13 (10), 2265-2270 (2003)
JOURNAL MEDLINE 12975309
PUBMED 12975309
REFERENCE 2 (bases 1 to 570)
AUTHORS Clark,H.F.
Direct Submission
JOURNAL Submitted (01-AUG-2003) Department of Bioinformatics, Genentech,
Inc., 1 DNA Way, South San Francisco, CA 94080, USA
FEATURES
Location/Qualifiers
1. .570
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/mol_type="mRNA"
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gene

1. .570
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79. .393
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VG"

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79. .393
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ORIGIN
Query Match 99.0%; Score 308.8; DB 9; Length 570;
Best Local Similarity 99.4%; Pred. No. 5.7e-39;
Matches 310; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

1 ATGAAGCTCGCGCGCTCTCTGGGGCTCTGCGTGGCGCTCTGCTGAGCTCGCTGCTGCT 60
79 ATGAAGCTCGCGCGCTCTCTGGGGCTCTGCGTGGCGCTCTGCTGAGCTCGCTGCTGCT 138
61 TTCTTAGTGGCTCGCGCAAGCTCTGCGCCAGCTCTGCTGCGCTGCTGAGTGGCGGCG 120
139 TTCTTAGTGGCTCGCGCAAGCTCTGCGCCAGCTCTGCTGCGCTGCTGAGTGGCGGCG 198
121 GAGCGCGCGCGCGCAAGCTCTGCGCCAGCTCTGCGCCAGCTCTGCGCCAGCTCTGCTG 180
199 GAGCGCGCGCGCGCAAGCTCTGCGCCAGCTCTGCGCCAGCTCTGCGCCAGCTCTGCTG 258
181 CTGAGCAGCTCGCGCATCCCTGCAACCTCTGAGGGCTCTGAGGGCTCTGAGGGCTCTG 240
259 CTGAGCAGCTCGCGCATCCCTGCAACCTCTGAGGGCTCTGAGGGCTCTGAGGGCTCTG 318
241 GAGCTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 300
319 GAGCTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 378
301 ACAGTGTGTTGGC 312
379 ACAGTGTGTTGGC 390

RESULT 13
AF313458
LOCUS Homo sapiens UGRP2 mRNA, complete cds.
DEFINITION AF313458
ACCESSION AF313458
VERSION AF313458.1 GI:16555421
KEYWORDS Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 347)
AUTHORS Niimi,T., Keck-Waggoner,C.L., Popescu,N.C., Zhou,Y., Levitt,R.C.
and Kimura,S.
UGRP1, a uteroglobin/Clara cell secretory protein-related protein,
is a novel lung-enriched downstream target gene for the
T/EBP/NKX2.1 homeodomain transcription factor
Mol. Endocrinol. 15 (11), 2021-2036 (2001)
JOURNAL MEDLINE 21539178
PUBMED 11682631
REFERENCE 2 (bases 1 to 347)
AUTHORS Niimi,T., Copeland,N.G., Gilbert,D.J., Jenkins,N.A., Srisodasai,A.,
Zimonjic,D.B., Keck-Waggoner,C.L., Popescu,N.C. and Kimura,S.
Cloning, expression, and chromosomal localization of the mouse gene
(Scgb3a1, alias Ugrp2) that encodes a member of the novel
uteroglobin-related protein gene family
Cytogenet. Genome Res. 97 (1-2), 120-127 (2002)
JOURNAL MEDLINE 12438750
PUBMED 12438750
REFERENCE 3 (bases 1 to 347)
AUTHORS Niimi,T. and Kimura,S.
Direct Submission
TITLE
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JOURNAL Submitted (16-OCT-2000) Laboratory of Metabolism, National Cancer Institute, NIH, 9000 Rockville Pike, Bethesda, MD 20892, USA

FEATURES

source 1. .347  
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 Db 11 ATGAAGTGGCGCCCTCTGGGCTCTGGCTGGCCCTGCTCAGCTCGCTCGTGCT 70  
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 CY 121 GAGCGCGGCGCGGAGCCTGGCCAAACCCCTCGCCACCTCAACCGCTGAAGCTCTG 180  
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 Db 131 GAGCGCGGCGCGGAGCCTGGCCAAACCCCTCGCCACCTCAACCGCTGAAGCTCTG 190  
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 Db 251 GAGCTGGTCCCGAGGCGTGGGGCCGCTGAAGCCCTGAAGGCCCTGCTGGGGCCCTG 310  
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 Db 311 ACAGTGTGTGGC 322  
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RESULT 14  
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 DEFINITION AC108083  
 AC108083.1 GI:18369929  
 HTG; HTGS PHASE1; HTGS\_DRAFT; HTGS\_ACTIVEFIN.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 1 (bases 1 to 130129)  
 DOE Joint Genome Institute.  
 Sequencing of Human Chromosome 5  
 Unpublished  
 2 (bases 1 to 130129)  
 DOE Joint Genome Institute.  
 Direct Submission  
 Submitted (25-JAN-2002) Production Sequencing Facility, DOE Joint  
 Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA  
 -----Genome Center  
 Center: Joint Genome Institute  
 Center Code: JGI  
 Web site: <http://www.jgi.doe.gov>  
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 Project Information

Center Project Name: 632820  
 Center clone name: CITB-H1\_2013L15  
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 Summary Statistics  
 Consensus quality: 124488 bases at least Q40  
 Consensus quality: 128031 bases at least Q30  
 Consensus quality: 128842 bases at least Q20  
 Estimated insert size: 135000; agarose-fp estimation  
 Estimated insert size: 129829; sum-of-contigs estimation  
 Quality coverage: 7.66 in Q20 bases; agarose-fp estimation  
 Quality coverage: 7.97 in Q20 bases; sum-of-contigs estimation.  
 \* NOTE: This is a 'working draft' sequence. It currently  
 \* consists of 4 contigs. The true order of the pieces  
 \* is not known and their order in this sequence record is  
 \* arbitrary. Gaps between the contigs are represented as  
 \* runs of N, but the exact sizes of the gaps are unknown.  
 \* This record will be updated with the finished sequence.  
 \* as soon as it is available and the accession number will  
 \* be preserved.

4320: contig of 4320 bp in length  
 4321 4420: gap of unknown length  
 4421 23712: contig of 19292 bp in length  
 23713 23812: gap of unknown length  
 23813 48602: contig of 24790 bp in length  
 48603 48702: gap of unknown length  
 48703 130129: contig of 81427 bp in length.

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ORIGIN

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 AC106813.3 GI:19224876  
 HTG; HTGS PHASE2; HTGS\_DRAFT; HTGS\_ACTIVEFIN.  
 KEYWORDS Homo sapiens (human)  
 SOURCE Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

## REFERENCE

AUTHORS  
TITLE  
JOURNAL  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT

1 (bases 1 to 166777)  
DOE Joint Genome Institute.  
Sequencing of Human Chromosome 5  
Unpublished  
2 (bases 1 to 166777)  
DOE Joint Genome Institute.  
Direct Submission  
Submitted (12-JAN-2002) Production Sequencing Facility, DOE Joint  
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA  
3 (bases 1 to 166777)  
DOE Joint Genome Institute.  
Direct Submission  
Submitted (07-MAR-2002) Production Sequencing Facility, DOE Joint  
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA  
On Mar 7, 2002 this sequence version replaced gi:18369924.

## -----Genome Center

Center: Joint Genome Institute  
Center Code: JGI  
Web site: <http://www.jgi.doe.gov>

## -----

## Project Information

Center Project Name: 1519801  
Center clone name: RPCI-11\_58619

## -----

## Summary Statistics

Consensus quality: 163497 bases at least Q40  
Consensus quality: 166071 bases at least Q30  
Consensus quality: 166432 bases at least Q20  
Estimated insert size: 186250; agarose-fp estimation  
Quality coverage: 9.4 in Q20 bases; agarose-fp estimation  
Quality coverage: 10.51 in Q20 bases; sum-of-contigs estimation.  
\* NOTE: This is a 'working draft' sequence. It currently  
\* consists of 3 contigs. Gaps between the contigs  
\* are represented as runs of N. The order of the pieces  
\* is believed to be correct as given, however the sizes  
\* of the gaps between them are based on estimates that have  
\* been provided by the submitter.

\* This sequence will be replaced  
\* by the finished sequence as soon as it is available and  
\* the accession number will be preserved.

\* 1 62237: contig of 62237 bp in length  
\* 62238 62337: gap of unknown length  
\* 62338 75837: contig of 13500 bp in length  
\* 75838 75937: gap of unknown length  
\* 75938 166777: contig of 90840 bp in length.

## FEATURES

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## ORIGIN

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Best Local Similarity 98.8%; Pred No. 1.9e-28;  
Matches 240; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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120320 AGTCGGCGCGGAGCGCGGCGCGGACCTGGCGCAACCCCTCGGACCCCTCAACCGC 120379  
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170 TGAAGCTCTCTGTGAGCAGCTGGGCGATCCCGGTGAACCACTCATAGAGGCTCCCGA 229  
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120380 TGAAGCTCTCTGTGAGCAGCTGGGCGATCCCGGTGAACCACTCATAGAGGCTCCCGA 120439  
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230 AGTGTGTGGCTGAGCTGGGTCCCGCAGCGCGGTGGGGCGGTGAAGGCCCTGCG 289  
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Db 120440 AGTGTGTGGCTGAGCTGGGTCCCGCAGGCCGTGGGGCCGTGAAGGCCCTGCG 120499  
Qy 290 TGG 292  
Db 120500 TGG 120502  
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Search completed: June 6, 2004, 14:59:41  
Job time : 2270 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 6, 2004, 09:57:16 ; Search time 340 seconds  
(without alignments)  
3898.346 Million cell updates/sec

Title: US-10-081-817A-3

Perfect score: 312

Sequence: 1 atgaagctgcgcgcctcct.....gggcccctgacagtgttggc 312

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 3373863 seqs, 2124099841 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : N\_Geneseq\_29Jan04:\*

- 1: Geneseqn1980s:\*
- 2: Geneseqn1980s:\*
- 3: Geneseqn2000s:\*
- 4: Geneseqn2001as:\*
- 5: Geneseqn2001bs:\*
- 6: Geneseqn2002s:\*
- 7: Geneseqn2003as:\*
- 8: Geneseqn2003bs:\*
- 9: Geneseqn2003cs:\*
- 10: Geneseqn2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	308.8	99.0	519	2	AAV54621 LU105 pol
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3	308.8	99.0	543	3	Aaz298173 Human sig
4	308.8	99.0	561	9	Ade39936 Human lun
5	308.8	99.0	562	2	AAV54620
6	308.8	99.0	569	6	ABK40267
7	308.8	99.0	570	3	AAZ65103
8	308.8	99.0	570	5	AAF44249
9	308.8	99.0	570	7	ABX77974
10	308.8	99.0	570	7	ABX80386
11	308.8	99.0	570	7	ACA69292
12	308.8	99.0	570	7	ABX90363
13	308.8	99.0	570	7	ABX64209
14	308.8	99.0	570	7	ACA64431
15	308.8	99.0	570	7	ABX80890
16	308.8	99.0	570	7	ACD44399
17	308.8	99.0	570	7	ABX79570
18	308.8	99.0	570	7	ACA93591
19	308.8	99.0	570	7	ABX81273
20	308.8	99.0	570	7	ACA93089
21	308.8	99.0	570	7	ABX117173
22	308.8	99.0	570	8	ACA68028
23	308.8	99.0	570	8	ACA88477

#### ALIGNMENTS

##### RESULT 1

AAV54621 ID AAV54621 standard; cDNA; 519 BP.

XX AC AAV54621;

XX DT 25-MAR-2003 (revised)

XX DT 30-OCT-1998 (first entry)

XX LU105 polypeptide encoding cDNA clone 13278361H.

XX LU105; lung disease marker; immunoassay; lung disease; cancer; blood; plasma; serum; ss.

XX OS Homo sapiens.

XX Key Location/Qualifiers

XX CDS 79..393

XX FT /\*\*tag=a

XX FT /transl\_except= (pos:136..138, aa:Val)

XX FT /product= "LU105 polypeptide"

XX PN WO9833926-A1.

XX PD 06-AUG-1998.

XX PF 30-JAN-1998; 98WO-US001766.

XX PR 31-JAN-1997; 97US-00791710.

XX PA (ABBO ) ABBOTT LAB.

XX PI Billing-Medel PA, Cohen M, Colpitts TL, Friedman PN, Gordon J;

XX PI Granados EN, Hodges SC, Klass MR, Kratochvil JD, Robertsrap L;

XX PI Russell JC, Stroupe SD;

XX DR WPI; 1998-437479/37.

XX DR P-PSDB; AAW75868.

XX New nucleic acid for the lung disease marker LU105 - polypeptides, antibodies and genes, used for diagnosis, prevention, treatment of lung disease, specifically cancer.

XX PS Claim 11; Fig 1; 123pp; English.

XX Sequences shown in AAV54616 to AAV54621 represent LU105 specific

ACd81984 cDNA enco  
Ada37918 Human cDN  
Ada21604 Human cDN  
Ada10391 Human cDN  
Ada17935 cDNA enco  
Ada28043 Human cDN  
Ada94623 Human cDN  
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Ada92969 Human cDN  
Ach65545 Human cDN  
Ada2530 Human cDN  
AcD39535 Human cDN  
Ada06696 Human sec  
Ada39389 Human cDN  
Adb96415 Human PRO  
Adc57887 Human PRO  
Adc55251 Human PRO  
Adc12118 Human cDN  
Adc56540 Human PRO  
Adc07595 Human cDN  
Adc11585 Human cDN  
Adc14707 Novel hum

polynucleotide sequences. These are used in the method of the invention for detecting target LUI05 nucleic acid. The method comprises treating a sample with at least one LUI05 specific nucleic acid, or its complement which is at least 50 percent identical with the LUI05 specific nucleic acid sequences (AAV54616 to AAV54621). LUI05 is a lung disease marker. Cells transformed with a recombinant expression system that contains LUI05 specific nucleic acid fragments, are used to express recombinant LUI05 polypeptides which are used to raise antibodies. The antibodies are used to detect the LUI05 antigen, and correspondingly this antigen is used to detect specific antibodies, in usual immunoassays. The LUI05 polypeptides and nucleic acid sequences are used for diagnosis, staging, monitoring, prognosis, prevention, treatment and determination of susceptibility to, lung disease, specifically cancer. The LUI05 polypeptides are also used to screen for specific binding agents, useful therapeutically. LUI05 is a marker for lung disease (present at high concentration, in altered form or in an unusual body compartment) LUI05 can be detected in blood, plasma or serum in an inexpensive, non-invasive test. (Updated on 25-MAR-2003 to correct PI field.)

Sequence 519 BP; 78 A; 190 C; 170 G; 81 T; 0 U; 0 Other;

Query Match 99.0%; Score 308.8; DB 2; Length 519;  
Best Local Similarity 99.4%; Pred. No. 4.3e-53;  
Matches 310; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 ATGAAGCTCGCGCCCTCTCGGGCTCTGCGTGGCCCTGTCTGCAGCTCGCTCGTGTCT 60  
Db 79 ATGAAGCTCGCGCCCTCTCGGGCTCTGCGTGGCCCTGTCTGCAGCTCGCTCGTGTCT 138  
Qy 61 TTCTTAGTGGCTCGGCCAAGCTGTGCCCCAGCTGTGCTGCTGCTGAGTTCGGGCG 120  
Db 139 TTCTTAGTGGCTCGGCCAAGCTGTGCCCCAGCTGTGCTGCTGAGTTCGGGCG 198  
Qy 121 GAGCCCGGGCGGGAGCCCTGGCCAAACCCCTCGGCACCCCTCAACCCGCTGAAGCTCTG 180  
Db 199 GAGCCCGGGCGGGAGCCCTGGCCAAACCCCTCGGCACCCCTCAACCCGCTGAAGCTCTG 258  
Qy 181 CTGAGCAGCTGGGCATCCCTGTGAACACCTCATAGAGGCTCCCGAAGTGTGTGGCT 240  
Db 259 CTGAGCAGCTGGGCATCCCTGTGAACACCTCATAGAGGCTCCCGAAGTGTGTGGCT 318  
Qy 241 GAGTGGTCCCGAGGCGTGGGGCGCTGAAGCCCTGAAGGCCCTGCTGGGGCGCTG 300  
Db 319 GAGTGGTCCCGAGGCGTGGGGCGCTGAAGCCCTGAAGGCCCTGCTGGGGCGCTG 378  
Qy 301 ACAGTGTGTGGC 312  
Db 379 ACAGTGTGTGGC 390

RESULT 2  
AAZ29723  
ID AAZ29723 standard; DNA; 543 BP.

AC AAZ29723;  
XX  
XX 27-MAR-2000 (first entry)  
DT  
XX Human lung specific gene Lngl07.

DE  
XX Lung Specific Gene; LSG; Lngl07; human; diagnostic marker; prognosticate;  
KW lung cancer; diagnosis; ds.  
XX  
XX Homo sapiens.

OS  
FH Key Location/Qualifiers  
FT CDS 93..407  
FT FT /\*tag= a  
FT FT /product= "LSG Lngl07 protein"  
XX  
XX

W09960160-A1.

PD 25-NOV-1999.

XX 12-MAY-1999; 99WO-US010344.  
PF  
XX 21-MAY-1998; 98US-0086212P.  
PR  
XX (DIAD-) DIADEXUS LLC.  
PA  
XX Yang F, Macina RA, Sun Y;  
PI  
XX WPI; 2000-116320/10.  
DR  
XX P-PSDB; AAY44458.  
DR  
XX A new method for diagnosing, monitoring and staging lung cancer.  
XX  
XX Claim 6; Page 36; 40pp; English.  
XX  
XX The present sequence is a lung specific gene (LSG) Lngl07 from human  
CC clone ID 586271. The LSG has high level of tissue specificity for lungs  
CC and is overexpressed in cancerous tissues. The sequence serves as a  
CC diagnostic marker for detecting, monitoring, staging and prognosticating  
CC lung cancer. The diagnosis involves comparing levels of LSG in samples  
CC obtained from patient and normal control  
XX  
XX Sequence 543 BP; 89 A; 194 C; 178 G; 82 T; 0 U; 0 Other;

Query Match 99.0%; Score 308.8; DB 3; Length 543;  
Best Local Similarity 99.4%; Pred. No. 4.3e-53;  
Matches 310; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 ATGAAGCTCGCGCCCTCTCGGGCTCTGCGTGGCCCTGTCTGCAGCTCGCTCGTGTCT 60  
Db 93 ATGAAGCTCGCGCCCTCTCGGGCTCTGCGTGGCCCTGTCTGCAGCTCGCTCGTGTCT 152  
Qy 61 TTCTTAGTGGCTCGGCCAAGCTGTGCCCCAGCTGTGCTGCTGAGTTCGGGCG 120  
Db 153 TTCTTAGTGGCTCGGCCAAGCTGTGCCCCAGCTGTGCTGCTGAGTTCGGGCG 212  
Qy 121 GAGCCCGGGCGGGAGCCCTGGCCAAACCCCTCGGCACCCCTCAACCCGCTGAAGCTCTG 180  
Db 213 GAGCCCGGGCGGGAGCCCTGGCCAAACCCCTCGGCACCCCTCAACCCGCTGAAGCTCTG 272  
Qy 181 CTGAGCAGCTGGGCATCCCTGTGAACACCTCATAGAGGCTCCCGAAGTGTGTGGCT 240  
Db 273 CTGAGCAGCTGGGCATCCCTGTGAACACCTCATAGAGGCTCCCGAAGTGTGTGGCT 332  
Qy 241 GAGTGGTCCCGAGGCGTGGGGCGCTGAAGCCCTGAAGGCCCTGCTGGGGCGCTG 300  
Db 333 GAGTGGTCCCGAGGCGTGGGGCGCTGAAGGCCCTGCTGGGGCGCTG 392  
Qy 301 ACAGTGTGTGGC 312  
Db 393 ACAGTGTGTGGC 404

RESULT 3  
AAZ98173  
ID AAZ98173 standard; cDNA; 543 BP.

XX AAZ98173;  
XX

XX 11-MAY-2000 (first entry)

DE Human signal peptide containing protein HSPP-65 cDNA SEQ ID NO:199.

XX Human; signal peptide-containing protein; HSPP; diagnosis; cancer;  
KW inflammation; cardiovascular disease; anticancer; anti-inflammatory;  
KW antimicrobial; nootropic; neuroprotective; cardiovascular; hepatotropic;  
KW antiasthmatic; gene therapy; cell proliferation; neurological disorder;  
KW reproductive disorder; developmental disorder; arteriosclerosis;  
KW cirrhosis; psoriasis; acquired immune deficiency syndrome; anaemia;  
KW asthma; Crohn's disease; infection; Alzheimer's disease; schizophrenia;  
KW Parkinson's disease; Huntington's diseases; ovulatory defect;  
KW muscular dystrophy; ss.





Db	237	GAGCGCGGGCGGACCCCTGGCCAAACCCCTCGGCACCCCTCAACCCGCTGAAGTCTCTG	299
Qy	181	CTGAGCAGCCTGGGCATCCCGCTGAACCACTCATAGAGGGCTCCAGAAAGTGTGTGGCT	240
Db	297	CTGAGCAGCCTGGGCATCCCGCTGAACCACTCATAGAGGGCTCCAGAAAGTGTGTGGCT	356
Qy	241	GAGCTGGTCCCGCAGGCCGTGGGGCCGTGAAGGCCCTGAAGGCCCTGCTGGGGGCCCTG	300
Db	357	GAGCTGGTCCCGCAGGCCGTGGGGCCGTGAAGGCCCTGAGAGGCCCTGCTGGGGGCCCTG	416
Qy	301	ACAGTGTGTTGGC 312	
Db	417	ACAGTGTGTTGGC 428	
RESULT 5			
AAV54620			
ID	AAV54620 standard; cDNA; 562 BP.		
XX	AAV54620;		
XX	25-MAR-2003 (revised)		
DT	30-OCT-1998 (first entry)		
XX	LUI05 specific consensus polynucleotide sequence.		
XX	LUI05; lung disease marker; immunoassay; lung disease; cancer; blood;		
KW	plasma; serum; ss.		
XX	Homo sapiens.		
OS			
XX	Key		
XX	Location/Qualifiers		
FT	122..436		
FT	/*tag= a		
FT	/transl_except= (pos:176..178, aa:Val)		
FT	/product= "LUI05 polypeptide"		
XX			
PN	WO9833926-A1.		
XX			
PD	06-AUG-1998.		
XX			
PF	30-JAN-1998; 98WO-US001766.		
XX			
PR	31-JAN-1997; 97US-00791710.		
XX			
PA	(ABBO ) ABBOTT LAB.		
PI	Billing-Medel PA, Cohen M, Colpitts TL, Friedman PN, Gordon J;		
PI	Granados EN, Hodges SC, Klass MR, Kratochvil JD, Robertsrap L;		
PI	Russell JC, Sroupe SB;		
XX	WPI; 1998-437479/37.		
DR	P-PSDB; AAV75868.		
XX			
PT	New nucleic acid for the lung disease marker LUI05 - polypeptides,		
PT	antibodies and genes, used for diagnosis, prevention, treatment of lung		
PT	disease, specifically cancer.		
XX			
PS	Claim 11; Fig 1; 123pp; English.		
XX			
CC	Sequences shown in AAV54616 to AAV54621 represent LUI05 specific		
CC	polynucleotide sequences. These are used in the method of the invention		
CC	for detecting target LUI05 nucleic acid. The method comprises treating a		
CC	sample with at least one LUI05 specific nucleic acid, or its complement		
CC	which is at least 50 percent identical with the LUI05 specific nucleic		
CC	acid sequences (AAV54616 to AAV54621). LUI05 is a lung disease marker.		
CC	Cells transformed with a recombinant expression system that contains		
CC	LUI05 specific nucleic acid fragments, are used to express recombinant		
CC	LUI05 polypeptides which are used to raise antibodies. The antibodies are		
CC	used to detect the LUI05 antigen, and correspondingly this antigen is		
CC	used to detect specific antibodies, in usual immunoassays. The LUI05		
CC	polypeptides and nucleic acid sequences are used for diagnosis, staging,		
CC	monitoring, prognosis, prevention, treatment and determination of		

CC susceptibility to, lung disease, specifically cancer. The LU105  
CC polypeptides are also used to screen for specific binding agents, useful  
CC therapeutically. LU105 is a marker for lung disease (present at high  
CC concentration, in altered form or in an unusual body compartment). LU105  
CC can be detected in blood, plasma or serum in an inexpensive, non-invasive  
CC test. (Updated on 25-MAR-2003 to correct PI field.)

XX  
SQ Sequence 562 BP; 82 A; 200 C; 192 G; 86 T; 0 U; 2 Other;

Query Match 99.0%; Score 308.8; DB 2; Length 562;  
Best Local Similarity 99.4%; Pred. No. 4.3e-53;  
Matches 310; Conservative 0; Mismatches 2; Indels 0; Gaps 0

QY 1 ATGAAGCTCGCGCGCCCTCCTGGGGCTCTGGCTGGCCCTGTCTCTGCAGCTCCGCTCGTGT 60  
Db 122 ATGAAGCTCGCGCGCCCTCCTGGGGCTCTGGCTGGCCCTGTCTCTGCAGCTCCGCTGTGT 181

QY 61 TTCTTAGTGGGCTCGGCCACGCTGTGGCCAGCCTGTCTCTCGTGAGTCGGCGCG 120  
Db 182 TTCTTAGTGGGCTCGGCCCAAGCCTGTGGCCAGCCTGTCTCTCGTGAGTCGGCGCG 241

QY 121 GAGGCGGGCGGCGACCTCTGGCCAAACCCCTCGGCACCTCAACCCGCTGAAGTCCCTG 180  
Db 242 GAGGCGGGCGGCGACCTCTGGCCAAACCCCTCGGCACCTCAACCCGCTGAAGTCCCTG 301

QY 181 CTGAGCAGCCTGGGCGATCCCGTGAAACACCTCATGAGGGCTCCACAGTGTGTGGCT 240  
Db 302 CTGAGCAGCCTGGGCGATCCCGTGAAACACCTCATGAGGGCTCCACAGTGTGTGGCT 361

QY 241 GAGCTGGGTCCCCAGGCGCGTGGGGCCGCTGAAGGCCCTGTGGGGGGCCCTG 300  
Db 362 GAGCTGGGTCCCCAGGCGCGTGGGGCCGCTGAAGGCCCTGTGGGGGGCCCTG 421

QY 301 ACAGTGTGTGGC 312  
Db 422 ACAGTGTGTGGC 433

RESULT 6  
ID ABK40267  
XX ID ABK40267 standard; cDNA; 569 BP.  
XX AC ABK40267;  
XX AC  
XX DT  
XX DT  
XX DT  
DE cDNA encoding human PRO1245 polypeptide.  
XX Human; PRO; benign tumour; malignant tumour; lymphoid malignancy;  
XX leukaemia; neuronal disorder; stromal disorder; blastocoealic disorder;  
KW inflammatory disorder; immune disorder; angiogenic disorder;  
KW gene therapy; cytostatic; neuroprotective; gene; ss.  
OS Homo sapiens.  
PN  
XX WO200153486-A1.  
PN  
XX 26-JUL-2001.  
XX  
XX 11-FEB-2000; 2000WO-US003565.  
XX  
XX 08-MAR-1999; 99WO-US005028.  
XX 11-MAR-1999; 99US-0123972P.  
XX 11-MAY-1999; 99US-0133459P.  
XX 02-JUN-1999; 99WO-US012252.  
XX 22-JUN-1999; 99US-0140650P.  
XX 22-JUN-1999; 99US-0140653P.  
XX 20-JUL-1999; 99US-0144758P.  
XX 26-JUL-1999; 99US-0145698P.  
XX 28-JUL-1999; 99US-0146222P.  
XX 17-AUG-1999; 99US-0149395P.  
XX 31-AUG-1999; 99US-0151689P.  
XX 01-SEP-1999; 99WO-US020111.  
XX

PR 15-SEP-1999; 99WO-US021090.  
 PR 30-NOV-1999; 99WO-US028313.  
 PR 01-DEC-1999; 99WO-US028301.  
 PR 01-DEC-1999; 99WO-US028634.  
 PR 05-JAN-2000; 2000WO-US000219.  
 XX  
 PA (GETH ) GENENTECH INC.  
 XX  
 PI Ashkenazi AU, Goddard A, Godowski PJ, Gurney AL, Hillan KJ;  
 PI Marsters SA, Pan J, Pitti RM, Roy MA, Smith V, Stone DM;  
 PI Watanabe CK, Wood WI;  
 DR WPI; 2002-205567/26.  
 DR P-PSDB; AAU66141.  
 XX  
 PT Thirty five nucleic acids encoding PRO polypeptides, useful for treating  
 PT benign or malignant tumors, leukemias and lymphoid malignancies,  
 PT inflammatory, angiogenic and immunologic disorders.  
 XX  
 PS Claim 50; Fig 27; 302pp; English.  
 XX  
 CC The present invention relates to the isolation of novel human PRO  
 CC polypeptides and the polynucleotide sequences encoding them. The PRO  
 CC polypeptides, agonists, antagonists or anti-PRO antibodies are useful for  
 CC treating benign or malignant tumors (e.g. renal, kidney, bladder,  
 CC breast, etc), leukemias and lymphoid malignancies, other disorders such  
 CC as neuronal, glial, astrocytic, hypothalamic, glandular, macrophagal,  
 CC stromal and blastocoele disorders, inflammatory, immune and angiogenic  
 CC disorders. The polynucleotide sequences are also useful in gene therapy.  
 CC ABK40254-ABK40288 encode for the human PRO polypeptides of the invention  
 XX  
 SQ Sequence 569 BP; 128 A; 190 C; 170 G; 81 T; 0 U; 0 Other;

Query Match 99.0%; Score 308.8; DB 6; Length 569;  
 Best Local Similarity 99.4%; Pred. No. 4.3e-53;  
 Matches 310; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ATGAAGCTGGCGCCCTCTGGGGCTGTGGTGGCCCTGTGCTGAGCTCCGCTCGTGTCT 60  
 DB 79 ATGAAGCTGGCGCCCTCTGGGGCTGTGGTGGCCCTGTGCTGAGCTCCGCTCGTGTCT 138  
 QY 61 TTCTAGTGGCTCGGCAAGCTGTGGCCACCTGTGCTGCTGCTGAGTCCGCGGG 120  
 DB 139 TTCTAGTGGCTCGGCAAGCTGTGGCCACCTGTGCTGCTGAGTCCGCGGG 198  
 QY 121 GAGGCGGGGCGGGACCTTGGCCACCTTGGCCACCTTGGCCACCTTGGCCACCTTGG 180  
 DB 199 GAGGCGGGGCGGGACCTTGGCCACCTTGGCCACCTTGGCCACCTTGGCCACCTTGG 258  
 QY 181 CTGAGCAGCTGGGATCCCGTGAACACCTTGAAGGGCTCCAGAGTGTGTGGCT 240  
 DB 259 CTGAGCAGCTGGGATCCCGTGAACACCTTGAAGGGCTCCAGAGTGTGTGGCT 318  
 QY 241 GAGCTGGGTCCTGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 300  
 DB 319 GAGCTGGGTCCTGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 378  
 QY 301 ACAGTGTGTGGC 312  
 DB 379 ACAGTGTGTGGC 390

RESULT 7  
 ID AAZ65103  
 XX AAZ65103 standard; cDNA; 570 BP.  
 AC AAZ65103;  
 XX  
 DT 05-APR-2000 (first entry)  
 DE Membrane-bound protein PRO1245 encoding cDNA.  
 XX  
 KW Membrane-bound polypeptide; PRO polypeptide; LDL receptor; TIE ligand;

KW pharmaceutical; receptor immunoadhesin; gene mapping; ss.  
 XX Homo sapiens.  
 OS WO9963088-A2.  
 XX  
 XX 09-DEC-1999.  
 XX  
 XX 02-JUN-1999; 99WO-US012252.  
 XX  
 XX 02-JUN-1998; 98US-0087607P.  
 XX 02-JUN-1998; 98US-0087609P.  
 XX 02-JUN-1998; 98US-0087759P.  
 XX 03-JUN-1998; 98US-0087827P.  
 XX 04-JUN-1998; 98US-0088021P.  
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 XX 04-JUN-1998; 98US-0088030P.  
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 XX 05-JUN-1998; 98US-0088212P.  
 XX 09-JUN-1998; 98US-0088217P.  
 XX 10-JUN-1998; 98US-0088655P.  
 XX 10-JUN-1998; 98US-0088722P.  
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 XX 10-JUN-1998; 98US-0088734P.  
 XX 10-JUN-1998; 98US-0088738P.  
 XX 10-JUN-1998; 98US-0088740P.  
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 XX 10-JUN-1998; 98US-0088810P.  
 XX 10-JUN-1998; 98US-0088811P.  
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 XX 17-JUN-1998; 98US-0089653P.  
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 XX 18-JUN-1998; 98US-0089907P.  
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 XX 19-JUN-1998; 98US-0089947P.  
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 XX 19-JUN-1998; 98US-0089952P.  
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 XX 23-JUN-1998; 98US-0090254P.  
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 XX 24-JUN-1998; 98US-0090429P.  
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 XX 24-JUN-1998; 98US-0090461P.  
 XX 24-JUN-1998; 98US-0090472P.  
 XX 24-JUN-1998; 98US-0090535P.  
 XX 24-JUN-1998; 98US-0090538P.

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24-JUN-1998; 98US-0090540P.
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25-JUN-1998; 98US-0090676P.
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25-JUN-1998; 98US-0090688P.
25-JUN-1998; 98US-0090690P.
25-JUN-1998; 98US-0090691P.
25-JUN-1998; 98US-0090694P.
25-JUN-1998; 98US-0090695P.
25-JUN-1998; 98US-0090696P.
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01-JUL-1998; 98US-0091358P.
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02-JUL-1998; 98US-0091478P.
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18-AUG-1998; 98US-0097022P.
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26-AUG-1998; 98US-0097954P.
26-AUG-1998; 98US-0097955P.
26-AUG-1998; 98US-0097971P.
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26-AUG-1998; 98US-0097986P.
26-AUG-1998; 98US-0098014P.
31-AUG-1998; 98US-0098525P.
16-SEP-1998; 98US-0100634P.
12-JAN-1999; 98US-0115565P.

XX PA (GETH ) GENENTECH INC.
XX PI Baker K, Chen J, Goddard A, Gurney AL, Smith V, Watanabe CK;
XX PI Wood WI, Yuan J;
XX DR WPI; 2000-072883/06.
XX DR P-PSDB; AAY66757.
XX PT Membrane-bound proteins and related nucleotide sequences.
XX ES Claim 2; Fig 289; 822pp; English.
XX CC The invention provides membrane-bound PRO polypeptides and
CC polynucleotides encoding them. The PRO sequences of the invention were
CC identified based on extracellular domain homology screening. The PRO
CC sequences have homology with proteins including LDL receptors, TIE
CC ligands and various enzymes. The membrane-bound proteins and receptor
CC molecules are useful as pharmaceutical and diagnostic agents. Receptor
CC immunoadhesins, for instance, can be used as therapeutic agents to block
CC receptor-ligand interactions. The membrane-bound proteins can also be
CC employed for screening of potential peptide or small molecule inhibitors
CC of the relevant receptor/ligand interaction. The PRO encoding sequences
CC are useful as hybridization probes, in chromosome and gene mapping and in
CC the generation of antisense RNA and DNA. PRO nucleic acid sequences will
CC also be useful for the preparation of PRO polypeptides, especially by
CC recombinant techniques
XX SQ Sequence 570 BP; 129 A; 190 C; 170 G; 81 T; 0 U; 0 Other;
Query Match 99.0%; Score 308.8; DB 3; Length 570;
Best Local Similarity 99.4%; Pred. No. 4.3e-53;
Matches 310; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 1 ATGAAGCTCGCGCCCTCTGGGGCTCTGGTGGCCCTGTCCTGCGAGCTCGGCTCGTCTGCT 60
Db 79 ATGAAGCTCGCGCCCTCTGGGGCTCTGGTGGCCCTGTCCTGCGAGCTCGGCTCGTCTGCT 138
Qy 61 TTCTTAGTGGCTCGGCGCAAGCCTGTGGCCAGCCTGTCTGCTGCTGAGTGGGGCGG 120
Db 139 TTCTTAGTGGCTCGGCGCAAGCCTGTGGCCAGCCTGTGGCCAGCCTGTCTGCTGAGTGGGGCGG 198
Qy 121 GAGCCCGGGCGGGAGCCTTGGCCCAACCCCTCGGCACCCCTCAACCCGCTGAAGCTCCTG 180
Db 199 GAGCCCGGGCGGGAGCCTTGGCCCAACCCCTCGGCACCCCTCAACCCGCTGAAGCTCCTG 258
Qy 181 CTGAGCAGCTGGGCTCCCGGTGACCCCTCATAGAGGCTCCCAAGTGTGGCT 240
Db 259 CTGAGCAGCTGGGCTCCCGGTGACCCCTCATAGAGGCTCCCAAGTGTGGCT 318
Qy 241 GAGCTGGTCCCCAGGCGGTGGGGCGCGTGAAGGCCCTGAAGGCCCTGTGGGGGCCCTG 300
Db 319 GAGCTGGTCCCCAGGCGGTGGGGCGCGTGAAGGCCCTGAAGGCCCTGTGGGGGCCCTG 378
Qy 301 ACAGTGTGGC 312
Db 379 ACAGTGTGGC 390
RESULT 8
AAF44249
ID AAF44249 standard; cDNA; 570 BP.
XX AC AAF44249;
XX 02-APR-2001 (first entry)
DE Human PRO1245 (UNQ29) nucleotide sequence SEQ ID NO:407.
XX Human; secreted and transmembrane protein; PRO; cytostatic; cell death;
XX cancer; chromosomal mapping; gene mapping; tissue typing;
XX diagnostic assay; ss.
XX
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PR 30-NOV-1999; 98WO-US028313.  
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PR 16-DEC-1999; 98WO-US030095.  
PR 20-DEC-1999; 98WO-US030911.  
PR 05-JAN-2000; 2000WO-US0000219.  
PR 06-JAN-2000; 2000WO-US000376.  
PR 11-FEB-2000; 2000WO-US003565.  
PR 18-FEB-2000; 2000WO-US004341.  
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QY	241	GAGCTGGTTCOCAGGCGCTGCGGGCCGCTGAGAGGCCCTGTAAGGCCCTGCTGCGGGGCCCTTG 300
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DT	01-MAY-2003	(first entry)
XX	XX	
DE	Human secreted/transmembrane protein cDNA, #163.	
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KW	Human; gene; ss; PRO; secreted; transmembrane; signal peptide;	
KW	pharmaceutical; diagnostic; therapeutic; gene therapy.	
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XX	XX	
PN	US2002160384-A1.	
XX	XX	
PD	31-OCT-2002.	
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XX	14-NOV-2001;	2001US-00992598.
XX	16-JUN-1997;	97US-0049787P.
PR	17-OCT-1997;	97US-0062250P.
PR	05-NOV-1997;	97WO-US020069.
PR	12-NOV-1997;	97US-0065186P.
PR	13-NOV-1997;	97US-0065311P.
PR	24-NOV-1997;	97US-0066770P.
PR	25-FEB-1998;	98US-0075945P.
PR	20-MAR-1998;	98US-0078910P.
PR	28-APR-1998;	98US-0083322P.
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XX PA (GETH) GENENTECH INC.

XX PI Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;

XX PI Ferrara N, Fong S, Gerber H, Gerritsen ME, Goddard A, Godowski PJ;

XX PI Grimaldi JC, Gurney AL, Kljavin IJ, Napier MA, Pan J, Paoni NF;

XX PI Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM, Wood WI;

XX PI Zhang Z;

XX DR WPI; 2003-288106/28.

XX DR P-PSDB; ABU060604.

XX DR

XX PT New transmembrane polypeptides and nucleic acids encoding the

XX PT polypeptides, useful in gene therapy, in chromosome identification, as

XX PT chromosome markers, or in generating probes.

XX PT

XX PS Claim 2; Fig 289; 650pp; English.

XX PS

XX CC The invention discloses isolated PRO secreted/transmembrane polypeptides

XX CC comprising a sequence without signal peptide and the nucleic acid

XX CC encoding them. The polypeptides can be used to raise antibodies that

XX CC specifically bind to the PRO polypeptide, for linking a bioactive

XX CC molecule to a cell expressing a PRO protein and for modulating at least

XX CC one biological activity of a cell. The PRO polypeptides or

XX CC polynucleotides are also useful in gene therapy, in chromosome

XX CC identification, as chromosome markers, or in generating probes. The PRO

XX CC polypeptides are useful as molecular markers for protein electrophoresis,

XX CC and the isolated nucleic acids may be used for recombinantly expressing

XX CC those markers. The PRO polypeptides and nucleic acids may also be used in

XX CC tissue typing. Anti-PRO antibodies are useful in diagnostic assays for

XX CC PRO, and in affinity purification of PRO from recombinant cell culture or

XX CC natural sources. The sequences presented in ABX90468 are the

XX CC genes encoding, the primers amplifying and the probes detecting the PRO

XX CC polynucleotides of the invention. Note: The sequence data for this patent

XX CC is also available in electronic format from USPTO at

XX CC seqdata.uspto.gov/sequence.html

XX CC

XX SQ Sequence 570 BP; 129 A; 190 C; 170 G; 81 T; 0 U; 0 Other;

Query Match 99.0%; Score 308.8; DB 7; Length 570;

Best Local Similarity 99.4%; Pred. No. 4.3e-53;

Matches 310; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ATGAGCTCGCGCCCTCTCGGGCTCTGCGTGGCCCTCTGCTGAGCTCGCTCGTGTGCT 60

Db 79 ATGAGCTCGCGCCCTCTCGGGCTCTGCGTGGCCCTCTGCTGAGCTCGCTCGTGTGCT 138

QY 61 TTCTTAGTGGCTCGGCAAGCCCTGTGGCCAGCCCTGTGCTGGCTGGAGTGGCGGCG 120

Db 139 TTCTTAGTGGCTCGGCAAGCCCTGTGGCCAGCCCTGTGCTGGCTGGAGTGGCGGCG 198

QY 121 GAGCGCGGCGCGGACCTGTGGCCAAACCCCTCGGCAACCCCTCAACCGCTGAAGCTCTTG 180

Db 199 GAGCGCGGCGCGGACCTGTGGCCAAACCCCTCGGCAACCCCTCAACCGCTGAAGCTCTTG 258

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RESULT 13

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ID ABX64209 standard; cDNA; 570 BP.

XX XX

AC ABX64209;

XX DT 26-FEB-2003 (first entry)

XX DE cDNA encoding human PRO1245 polypeptide.

XX DE

XX KW Human; PRO polypeptide; secreted protein; transmembrane protein;

XX KW genetic disorder; antibacterial; immunosuppressive; transgenic;

XX KW gene therapy; gene; ss.

XX OS Homo sapiens.

XX PN US2002103125-A1.

XX PD 01-AUG-2002.

XX PF

XX PF 20-NOV-2001; 2001US-00989731.

XX PR 16-JUN-1997; 97US-0049787P.

XX PR 17-OCT-1997; 97US-0062250P.

XX PR 05-NOV-1997; 97WO-US020069.

XX PR 12-NOV-1997; 97US-0065186P.

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PR	09-JUL-2001;	2001WO-US021735;
PR	26-AUG-2001;	2001US-0094192;
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XX	(GETH ) GENENTECH LTD.	
PA		
XX	Ashkenazi AJ, Baker KP, B...	
XX	Ferrara N, Fong S, Gerber H	
PI	Grimaldi JC, Gurney AL, Klj	
PI	Roy MA, Stewart TA, Tumas	
PI	Zhang Z;	
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Dd	319 GAGCTGGGTCCCAGGCCGTGGGGCCGCTGAAGGCCCTCTGAAGGCCCTGTGGGGGCCCTG 378 
QY	301 ACAGTGTTTGGC 312 
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XC	
AA	ACA64431;
DT	17-JUN-2003 (first entry)
DE	Novel human secreted and transmembrane protein PRO1245 cDNA.
XX	Human; secreted and transmembrane protein; cytostatic; anti-HIV; virucide; hepatotropic; antiinflammatory; neuroprotective; gene therapy; PRO; pharmaceutical; diagnostic; biosensor; bioeffector; malignancy; cancer; ovarian cancer; colorectal cancer; Kaposi's sarcoma; leukaemia; lymphoma; hepatitis B; multiple sclerosis; Crohn's disease; drug screening; gene; ss.
OS	Homo sapiens.
XX	
PN	US2003003531-A1.
PX	
PD	02-JAN-2003.
XX	
PF	19-NOV-2001; 2001US-00989734.
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PR	16-JUN-1997; 97US-0049787P.
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PR	13-NOV-1997; 97US-0065311P.
PR	24-NOV-1997; 97US-0066770P.
PR	25-FEB-1998; 98US-0075945P.
PR	20-MAR-1998; 98US-CO78910P.
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PR	28-MAY-1998; 98US-CO87106P.
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PR 10-JUN-1998; 98US-0088824P.
PR 10-JUN-1998; 98US-0088826P.
PR 11-JUN-1998; 98US-0088858P.
PR 11-JUN-1998; 98US-0088861P.
PR 11-JUN-1998; 98US-0088876P.
PR 12-JUN-1998; 98US-0089105P.
PR 16-JUN-1998; 98US-0089440P.
PR 16-JUN-1998; 98US-0089512P.
PR 16-JUN-1998; 98US-0089514P.
PR 17-JUN-1998; 98US-0089532P.
PR 17-JUN-1998; 98US-0089538P.
PR 17-JUN-1998; 98US-0089598P.
PR 17-JUN-1998; 98US-0089599P.
PR 17-JUN-1998; 98US-0089600P.
PR 17-JUN-1998; 98US-0089653P.
PR 18-JUN-1998; 98US-0089801P.
PR 18-JUN-1998; 98US-0089807P.
PR 18-JUN-1998; 98US-0089907P.
PR 16-SEP-1998; 98WO-US019330.
PR 17-SEP-1998; 98WO-US019437.
PR 07-OCT-1998; 98WO-US021141.
PR 01-DEC-1998; 98WO-US025108.
PR 05-JAN-1999; 99WO-US000106.
PR 08-MAR-1999; 99WO-US005028.
PR 02-JUN-1999; 99WO-US012252.
PR 15-SEP-1999; 99WO-US021090.
PR 18-SEP-1999; 99WO-US021547.
PR 30-NOV-1999; 99WO-US028313.
PR 01-DEC-1999; 99WO-US028301.
PR 01-DEC-1999; 99WO-US028634.
PR 16-DEC-1999; 99WO-US030095.
PR 20-DEC-1999; 99WO-US030911.
PR 05-JAN-2000; 2000WO-US000219.
PR 06-JAN-2000; 2000WO-US000376.
PR 11-FEB-2000; 2000WO-US003565.
PR 18-FEB-2000; 2000WO-US004341.
PR 22-FEB-2000; 2000WO-US004414.
PR 24-FEB-2000; 2000WO-US004914.
PR 24-FEB-2000; 2000WO-US005004.
PR 02-MAR-2000; 2000WO-US005841.
PR 10-MAR-2000; 2000WO-US006319.
PR 15-MAR-2000; 2000WO-US006884.
PR 20-MAR-2000; 2000WO-US007377.
PR 30-MAR-2000; 2000WO-US008439.
PR 15-MAY-2000; 2000WO-US013358.
PR 17-MAY-2000; 2000WO-US013705.
PR 22-MAY-2000; 2000WO-US014042.
PR 30-MAY-2000; 2000WO-US014941.
PR 02-JUN-2000; 2000WO-US015264.
PR 28-JUL-2000; 2000WO-US020710.
PR 11-AUG-2000; 2000WO-US022031.
PR 23-AUG-2000; 2000WO-US023522.
PR 24-AUG-2000; 2000WO-US023328.
PR 08-NOV-2000; 2000WO-US030952.
PR 01-DEC-2000; 2000WO-US032678.
PR 28-FEB-2001; 2001WO-US006520.
PR 01-JUN-2001; 2001WO-US017800.

PR 20-JUN-2001; 2001WO-US019692.
PR 29-JUN-2001; 2001WO-US021066.
PR 09-JUL-2001; 2001WO-US021735.
PR 28-AUG-2001; 2001US-00941992.
XX (GETH ) GENENTECH INC.
XX Ashkenazi AJ, Baker KP, Botstein D, Desnovers L, Eaton DL;
PI Ferrara N, Fong S, Gerber H, Gerritsen ME, Goddard A, Godowski RJ;
PI Grimaldi JC, Gurney AL, Kijavini LJ, Napier MA, Pan J, Paoni NF;
PI Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM, Wood WI;
PI Zhang Z;
XX WPI; 2003-352829/33.
DR P-PSDB; ABU72571.
XX
PT New genes and secreted and transmembrane polypeptides (e.g. PRO183 or
PT PRO184), useful for treating or diagnosing e.g. ovarian cancer, Kaposi's
PT sarcoma, leukemia, lymphoma, hepatitis B, multiple sclerosis or Crohn's
PT disease.
XX
PS Claim 1; Fig 289; 563pp; English.
XX
CC The invention describes a new isolated nucleic acid molecule comprising
CC the full length coding sequence of the DNA deposited with the American
CC Type Culture Collection (e.g. ATCC Deposit No. 209621, 552-PTA, 819-PTA,
CC 209439, 203135, etc); or a sequence with at least 80% identity to a DNA
CC encoding a PRO polypeptide. The PRO polypeptides or polynucleotides are
CC useful as pharmaceuticals, diagnostics, biosensors or bioreactors. These
CC are particularly useful for detecting or treating e.g. malignancies or
CC cancers (e.g. ovarian cancer, colorectal cancer, Kaposi's sarcoma,
CC leukemia or lymphoma), hepatitis B, multiple sclerosis, or Crohn's
CC disease in mammals. The PRO polypeptides are useful in drug screening,
CC particularly as targets for therapeutic intervention in these diseases,
CC and in the diagnostic determination of the presence of these diseases.
CC The PRO polypeptides are also useful as molecular weight markers, or for
CC chromosome identification. The PRO genes are useful as hybridisation
CC probes, or for screening libraries of human cDNA, genomic DNA or mRNA.
CC The PRO genes may also be used in gene therapy, particularly for
CC replacing a defective gene. This sequence encodes a novel human secreted
CC and transmembrane PRO polypeptide
XX
SQ Sequence 570 BP; 129 A; 190 C; 170 G; 81 T; 0 U; 0 Other;

Query Match 99.0%; Score 308.8; DB 7; Length 570;
Best Local Similarity 99.4%; Pred.No. 4.3e-53;
Matches 310; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ATGAAGCTCGCCGCCCTCTCTGGGGCTCTGGTGGCCCTCTCTCTGAGCTCGCTCGTGTCT 60
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Db 259 CTGAGCAGCTGGGGCATCCCGTGAAACCACTCATAGAGGGCTCCCAAGAGTGTGTGGCT 318
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QY 301 ACAGTGTTTTGGC 312
Db 379 ACAGTGTTTTGGC 390
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GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 6, 2004, 13:39:06 ; Search time 2499 Seconds  
(without alignments)  
3728.291 Million cell updates/sec

Title: US-10-081-817A-3

Perfect score: 312

Sequence: 1 atgaagctgcgcgcctcct.....gggcctgcacagtgtttggc 312

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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1: em\_estba:\*

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5: em\_estov:\*

6: em\_estpl:\*

7: em\_estro:\*

8: em\_hic:\*

9: gb\_est1:\*

10: gb\_est2:\*

11: gb\_hic:\*

12: gb\_est3:\*

13: gb\_est4:\*

14: gb\_est5:\*

15: em\_estfun:\*

16: em\_estom:\*

17: em\_gss\_hum:\*

18: em\_gss\_inv:\*

19: em\_gss\_pln:\*

20: em\_gss\_vrt:\*

21: em\_gss\_fun:\*

22: em\_gss\_nam:\*

23: em\_gss\_mus:\*

24: em\_gss\_pro:\*

25: em\_gss\_rod:\*

26: em\_gss\_phg:\*

27: em\_gss\_vrl:\*

28: gb\_gss1:\*

29: gb\_gss2:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	308.8	99.0	473	12	BM920793 AGENCOURT
2	308.8	99.0	473	12	BM920794 AGENCOURT
3	308.8	99.0	490	12	BM977626 UI-CF-EN1
4	308.8	99.0	496	12	BI818715 603037535

5	308.8	99.0	1004	12	BI769722
6	308.8	99.0	1059	13	BQ067622
7	308.8	99.0	1083	12	BM921624
8	307.2	98.5	550	10	AK974727
9	303.8	97.4	437	14	CB049699
10	299.8	96.1	472	12	BM977779
11	298.8	95.8	439	9	AI685860
12	297.8	95.4	961	12	BI819045
13	296.8	95.1	407	12	BI820788
14	296.8	95.1	416	12	BI490604
15	296.8	95.1	491	12	BI819014
16	296.8	95.1	496	12	BI819795
17	296.8	95.1	875	12	BI822360
18	296.8	95.1	880	12	BI489765
19	296.2	94.9	680	12	BI821791
20	290.8	93.2	424	9	AI333740
21	290.8	93.2	425	9	AI187341
22	286.8	91.9	885	12	BI824102
23	283.2	90.8	476	12	BI818534
24	281.8	90.3	413	9	AI745557
25	281.8	90.3	424	9	AI744099
26	276.6	88.7	416	10	BF221778
27	272.8	87.4	896	12	BI824919
28	268.8	86.2	420	9	AI936195
29	258.2	82.8	662	12	BM982112
30	258.2	82.8	711	12	BM982925
31	258.2	82.8	718	14	CA313307
32	258.2	82.8	731	12	BM980649
33	255.4	81.9	878	12	BI823159
34	254.8	81.7	1000	12	BI908998
35	246	78.8	378	9	AI634641
36	236.6	75.8	526	9	AA742697
37	220.4	70.6	427	14	W76414
38	214	68.6	435	14	CB049698
39	212.6	68.1	424	14	W77934
40	206.8	66.3	343	9	AA649864
41	202.4	64.9	887	12	BI818788
42	188.6	60.4	335	9	AA902200
43	186.6	59.8	323	10	BE707758
44	174	55.8	320	13	BU679439
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#### ALIGNMENTS

RESULT 1

BM920793

LOCUS

DEFINITION

AGENCOURT\_6705937 NTH\_MGC\_115 Homo sapiens

5', mRNA sequence.

ACCESSION

BM920793

VERSION

BM920793.1

KEYWORDS

EST.

SOURCE

Homo sapiens

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

NIH-MGC

NIH-MGC

NIH-MGC

NIH-MGC

NIH-MGC

NIH-MGC

NIH-MGC

NIH-MGC

NIH-MGC

NIH-MGC

NIH-MGC

473 bp mRNA linear EST 12-MAR-2002

5', mRNA sequence.

AGENCOURT\_6705937 NTH\_MGC\_115 Homo sapiens

5', mRNA sequence.

ACCESSION

BM920793

VERSION

BM920793.1

KEYWORDS

EST.

SOURCE

Homo sapiens

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

NIH-MGC

NIH-MGC

NIH-MGC

NIH-MGC

NIH-MGC

NIH-MGC

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NIH-MGC

## FEATURES

source

Location/Qualifiers  
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## ORIGIN

Query Match 99.0%; Score 308.8; DB 12; Length 473;  
 Best Local Similarity 99.4%; Pred. No. 2.4e-42;  
 Matches 310; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ATGAAGCTCGCGCCCTCTGGGCTCTGGCTGGCCCTGTCTGCAGCTCGCTCGTCT 60  
 Db 7 ATGAAGCTCGCGCCCTCTGGGCTCTGGCTGGCCCTGTCTGCAGCTCGCTCGTCT 66

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QY 181 CTGAGCAGCTCGGCAATCCCGTGAACACCTCATAGAGGCTCCAGAGTGTGCT 240  
 Db 187 CTGAGCAGCTCGGCAATCCCGTGAACACCTCATAGAGGCTCCAGAGTGTGCT 246

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QY 301 ACAGTGTGGC 312  
 Db 307 ACAGTGTGGC 318

## RESULT 2

BM920794

LOCUS

BM920794 473 bp mRNA linear EST 12-MAR-2002  
 AGENCOURT 6705953 NIH\_MGC\_115 Homo sapiens cDNA clone IMAGE:5752039  
 5', mRNA sequence.

ACCESSION

BM920794

VERSION

BM920794.1

KEYWORDS

EST.

SOURCE

Homo sapiens (human)

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 473)

NIH-MGC <http://mgi.nhl.nih.gov/>.Email: [cgabs-remail.nih.gov](mailto:cgabs-remail.nih.gov)

Tissue Procurement: Life Technologies, Inc.

cDNA Library Preparation: Life Technologies, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation.

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

## FEATURES

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## ORIGIN

Query Match 99.0%; Score 308.8; DB 12; Length 473;  
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QY 1 ATGAAGCTCGCGCCCTCTGGGCTCTGGCTGGCCCTGTCTGCAGCTCGCTCGTCT 60  
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QY 61 TTCTTAGTGGCTCGGCAAGCTGTGGCCAGCTGTGGCTGGCTGGCTGGCTGGCT 120  
 Db 67 TTCTTAGTGGCTCGGCAAGCTGTGGCCAGCTGTGGCTGGCTGGCTGGCTGGCT 126

QY 121 GAGCGCGGCGCGGACCTGTGGCCAAACCTCTCGGCACCTCAACCCGCTCAAGCTCCT 180  
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QY 181 CTGAGCAGCTCGGCAATCCCGTGAACACCTCATAGAGGCTCCAGAGTGTGCT 240  
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QY 301 ACAGTGTGGC 312  
 Db 307 ACAGTGTGGC 318

## RESULT 3

BM977626/c

LOCUS

BM977626 490 bp mRNA linear EST 21-FEB-2003  
 UI-CF-ENI-aef-o-13-0-UI.s1 UI-CF-ENI Homo sapiens cDNA clone  
 UI-CF-ENI-aef-o-13-0-UI 3', mRNA sequence.

ACCESSION

BM977626

VERSION

BM977626.1

KEYWORDS

EST.

SOURCE

Homo sapiens (human)

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 490)

Bonaldo, M.F., Lennon, G. and Soares, M.B.

Normalization and subtraction: two approaches to facilitate gene

discovery

Genome Res. 6 (9), 791-806 (1996)

97044477

8889548

PUBMED

COMMENT

Contact: McCray, PB

McCray Lab







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QY 181 CTGAGCAGCTGGGCAATCCCGTGAACCACTCATAGAGGCTCCAGAGTGTGTGGCT 240
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QY 301 ACAGTGTTTGGC 312
DB 323 ACAGTGTTTGGC 334

RESULT 7
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DEFINITION AGENCOURT 6707854 NIH_MGC_115 Homo sapiens cDNA clone IMAGE:5753142
5', mRNA sequence.
ACCESSION BM921624
VERSION BM921624.1 GI:19372003
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1083)
AUTHORS NIH-MGC http://mgi.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabbs-remail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM12788 row: h column: 07
High quality sequence stop: 486.
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male lung, age 27; and 1 male testis, age 69. Library is
oligo-dT primed and directionally cloned (EcoRV site is
destroyed upon cloning). Average insert size 1.8 kb,
insert size range 1-3 kb. Library is normalized and
enriched for full-length clones and was constructed by C.
Gruber (Invitrogen). Research Genetics tracking code
021. Note: this is a NIH_MGC Library."
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Query Match 99.0%; Score 308.8; DB 12; Length 1083;
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QY 1 ATGAGCTCGCGCCCTCCCTGGGCTGTGGTGGCCCTGTCTTGCAGCTCCGCTCGTGT 60
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QY 121 GAGCGCGGGCCGCGGACCTGTGGCCAAACCCCTCGGCACCCCTCAACCCGCTGAAGCTCCTG 180

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RESULT 8
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ACCESSION AW974727
VERSION AW974727.1 GI:8165915
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 550)
AUTHORS Hegde, P., Qi, R., Abernathy, K., Dharap, S., Gaspard, R., Gay, C.,
Holt, J. E., Saeed, A. I., Sharov, V., Lee, N. H., Yeaman, T. J. and
Quackenbush, J.
TITLE Assessment of gene expression patterns in a model of colon tumor
metastasis using a 15,200 element cDNA microarray
JOURNAL Unpublished (2000)
COMMENT Contact: John Quackenbush
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 3528
Fax: 301 838 0208
Email: johnq@tigr.org
Plate: 338
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DB 205 CTGAGCAGCTGGGCAATCCCGTGAACCACTCATAGAGGCTCCAGAGTGTGTGGCT 264
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VERSION   CB049699.1 GI:27787986
KEYWORDS EST.
SOURCE    Homo sapiens (human)
ORGANISM  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
           Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 437)
          NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
          National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
          Tumor Gene Index
          Unpublished (1997)
          Contact: Robert Strausberg, Ph.D.
          Email: cgapbs-remail.nih.gov
          cDNA Library Preparation:
          CDNA Library Arrayed by: The I.M.A.G.E. Consortium/LINL
          DNA Sequencing by: National Institutes of Health Intramural
          Sequencing Center (NISC)
          Clone distribution: NCI-CGAP clone distribution information can be
          found through the I.M.A.G.E. Consortium/LINL at:
          info@image.lni.gov
          Plate: L1AM8008 row: J column: 10
          Seq primer: M13RPI reverse primer (ABI).
FEATURES             Location/Qualifiers
     source           1..437
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:3271401"
                     /sex="male"
                     /dev_stage="adult"
                     /lab_host="DH10B"
                     /clone_lib="NCI_CGAP_Pr28"
                     /note="Organ: prostate; Vector: pT7T3-Pac (Pharmacia)
                     with a modified polylinker; Plasmid DNA from the
                     normalized library NCI CGAP Pr22 was prepared, and ss
                     circles were made in vitro. Following HAP purification,
                     this DNA was used as tracer in a subtractive hybridization
                     reaction. The driver was PCR-amplified cDNAs from a pool
                     of 5,000 clones made from the same library (clonoids
                     985608-986759, 1101192-1101959, and 1217928-1220615).
                     Subtraction by Bento Soares and M. Fatima Bonaldo."
ORIGIN
Query Match          97.4%; Score 303.8; DB 14; Length 437;
Best Local Similarity 99.3%; Pred. No. 1.7e-41;
Matches 305; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      6 GCTCGCCCTCTCTGGGCTCTGGTGGCCCTGCTCGCTGGAGTCCGGCGCGGAGGC 125
Db      10 GCTCGCCCTCTCTGGGCTCTGGTGGCCCTGCTCGCTGGAGTCCGGCGCGGAGGC 129
QY      66 AGTGGGCTCGGCCAAGCCTGTGGCCACCCCTGCTCGCTGGAGTCCGGCGCGGAGGC 125
Db      70 AGTGGGCTCGGCCAAGCCTGTGGCCACCCCTGCTCGCTGGAGTCCGGCGCGGAGGC 129
QY      126 CGGGCCCGGACCTTGGCCACCCCTCGGCACCCCTCAACCCGTGAAGCTCTCTGCTGAG 185
Db      130 CGGGCCCGGACCTTGGCCACCCCTCGGCACCCCTCAACCCGTGAAGCTCTCTGCTGAG 189
QY      186 CAGCTGGGCATCCCGCTGACACCCTCATAGAGGGCTCCAGAGTGTGTGGCTGAGCT 245

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Db      190 CAGCTGGGCATCCCGCTGAACCACTCATAGAGGGCTCCAGAGTGTGTGGCTGAGCT 249
QY      246 GGTTCCCGAGCCGCTGGGGCCGTGAAGGCCCTGAAGCCCTGCTGGGGCCCTGACAGT 305
Db      250 GGTCCCGAGCCGCTGGGGCCGTGAAGGCCCTGAAGCCCTGCTGGGGCCCTGACAGT 309
QY      306 GTTTGGC 312
Db      310 GTTTGGC 316

RESULT 10
BM977779
LOCUS   UI-CF-EN1-aef-n-17-0-UI.s1 UI-CF-EN1 Homo sapiens cDNA clone
DEFINITION UI-CF-EN1-aef-n-17-0-UI 3', mRNA sequence.
ACCESSION BM977779
VERSION   BM977779.1 GI:19596542
KEYWORDS EST.
SOURCE    Homo sapiens (human)
ORGANISM  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
           Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 472)
          Bonaldo, M.F., Lennon, G., and Soares, M.B.
          Normalization and subtraction: two approaches to facilitate gene
          discovery
          Genome Res. 6 (9), 791-806 (1996)
          97044477
          889548
          Contact: McCray, PB
          McCray Lab
          University of Iowa
          2024 University of Iowa Med Labs, Iowa City, IA 52242, USA
          Tel: 319 356 4866
          Fax: 319 356 7171
          Email: paul-mccray@uiowa.edu
          Tissue Procurement: Dr. M. J. Welsh, University of Iowa
          CDNA Library Preparation: Dr. M. Bento Soares, University of Iowa
          CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
          DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
          Clone Distribution: Researchers may obtain clones from Research
          Genetics (www.resgen.com) or from Open Biosystems
          (www.openbiosystems.com).
          Seq primer: M13 FORWARD
          POLYA=Yes
FEATURES             Location/Qualifiers
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                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="UI-CF-EN1-aef-n-17-0-UI"
                     /tissue_type="Primary Lung Cystic Fibrosis Epithelial
                     Cells"
                     /dev_stage="Adult"
                     /lab_host="DH10B (Life Technologies) (T1 phage resistant)"
                     /clone_lib="UI-CF-EN1"
                     /note="Organ: Lung; Vector: pT7T3-Pac (Pharmacia) with a
                     modified polylinker; Site 1: EcoR I; Site 2: Not I;
                     UI-CF-EN1 is a normalized cDNA library containing the
                     following tissue(s): Primary Lung Cystic Fibrosis
                     Epithelial Cells. The library was constructed according to
                     Bonaldo, Lennon and Soares, Genome Research, 6:791-806,
                     1996. First strand cDNA synthesis was primed with an
                     oligo-dT primer containing a Not I site. Double stranded
                     cDNA was ligated to an EcoR I adaptor, digested with Not
                     I, and cloned directionally into pT7T3-Pac vector. The
                     oligonucleotide used to prime the synthesis of
                     first-strand cDNA contains a library tag sequence that is
                     located between the Not I site and the (dT)18 tail. The
                     sequence tag for this library is CTGCTCAGGT.
                     TAG_TISSUE=Human Lung Epithelial Cell lines untreated LPS

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6hr to LPS 24h  
TAG LIB=UI-CF-EN1  
TAG\_SEQ=CTGCTCAGGT"

## ORIGIN

Query Match 96.1%; Score 299.8; DB 12; Length 472;  
Best Local Similarity 97.7%; Pred. No. 7.9e-41;  
Matches 304; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 ATGAAGCTCGCGCCCTCCCTGGGGCTCTGGTGGCCCTGCTGAGCTCCGCTCGTGGCT 60  
DB 458 ATGAAGCTCGCGCCCTCCCTGGGGCTCTGGTGGCCCTGCTGAGCTCCGCTCGTGGCT 399  
QY 61 TTCTTAGTGGGCTCGGCGAAGCCCTGTGGCCAGCTCTGCTGCTGGAGTGGGGGG 120  
DB 398 TTTTATAGTGGGCTCGGCGAAGCCCTGTGGCCAGCTCTGCTGCTGGAGTGGGGGG 399  
QY 121 GAGCGCGGGCGGGGACCTTGGCAACCCCTCGGACCCCTCAACCCGCTGAAGCTCTG 180  
DB 338 GAGCGCGGGCGGGGACCTTGGCAACCCCTCGGACCCCTCAACCCGCTGAAGCTCTG 279  
QY 181 CTGAGCAGCTGGGCACTCCCGCTGAACCACTCATAGAGGCTCCCAAGAGTGTGGCT 240  
DB 278 TTGAGCAGCTGGGCACTCCCGCTGAACCACTCATAGAGGCTCCCAAGAGTGTGGCT 219  
QY 241 GAGCTGGTCCCCAGGCGGTGGGGCGCGTGAAGGCCCTGAGGCGCTGCTGGGGCGCTG 300  
DB 218 GAGCTGGTCCCCAGGCGGTGGGGCGCGTGAAGGCCCTGAGGCGCTGCTGGGGCGCTG 159  
QY 301 ACAGTGTGG 311  
DB 158 ACAGTGTGG 148

## RESULT 11

AI685860/c  
LOCUS tt90f09.x1 NCI\_CGAP\_Pr28 Homo sapiens cDNA clone IMAGE:2248841 3',  
DEFINITION mRNA sequence.

ACCESSION AI685860.1 GI:4897154  
VERSION  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
REFERENCE 1 (bases 1 to 439)  
AUTHORS Mammalia; Euthera; Primates; Catarrhini; Hominiidae; Homo.  
TITLE NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.  
JOURNAL National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
COMMENT Tumor Gene Index  
Unpublished (1997)  
Contact: Robert Strausberg, Ph.D.  
Email: cgaps-r@mail.nih.gov  
Tissue Procurement: Michael J. Brownstein, M.D., Ph.D., Michael R.  
Emmert-Buck, M.D., Ph.D.

cDNA Library Preparation: M. Bento Soares, Ph.D.  
cDNA Library Arrayed by: Greg Lennon, Ph.D.  
DNA Sequencing by: Washington University Genome Sequencing Center  
Clone distribution: NCI-CGAP clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
[www-bio.llnl.gov/bbrp/image/image.html](http://www-bio.llnl.gov/bbrp/image/image.html)  
Seq primer: -40UP from Gibco.  
Location/Qualifiers  
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/db\_xref="taxon:9606"  
/clone="IMAGE:2248841"  
/sex="male"  
/dev stage="adult"  
/lab\_host="DH10B"  
/clone\_lib="NCI\_CGAP\_Pr28"  
/note="Organ: prostate; Vector: pT73D-Pac (Pharmacia)

## FEATURES

source  
1. .439  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:2248841"  
/sex="male"  
/dev stage="adult"  
/lab\_host="DH10B"  
/clone\_lib="NCI\_CGAP\_Pr28"  
/note="Organ: prostate; Vector: pT73D-Pac (Pharmacia)

## ORIGIN

Query Match 95.8%; Score 298.8; DB 9; Length 439;  
Best Local Similarity 99.3%; Pred. No. 1.1e-40;  
Matches 300; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 11 CCGCCCTCTCGGGGCTCTGCTGGCCCTGTCCTGAGCTCCGCTCGTGTCTTAGTGG 70  
DB 439 CCGCCCTCTCGGGGCTCTGCTGGCCCTGTCCTGAGCTCCGCTCGTGTCTTAGTGG 380  
QY 71 GCTCGGCCAAGCCTGTGGCCAGCCTGTGCTGCTGGAGTGGCGGCGAGGCGGGG 130  
DB 379 GCTCGGCCAAGCCTGTGGCCAGCCTGTGCTGCTGGAGTGGCGGCGAGGCGGGG 320  
QY 131 CCGGGACCTTGGCCACCCCTCGGCAACCCCTCAACCCGCTGAAGCTCTGCTGAGCAGCC 190  
DB 319 CCGGGACCTTGGCCACCCCTCGGCAACCCCTCAACCCGCTGAAGCTCTGCTGAGCAGCC 260  
QY 191 TGGGCATCCCGCTGAACCACTCATAGAGGCTCCCAAGAGTGTGGTGAAGTGGTGC 250  
DB 259 TGGGCATCCCGCTGAACCACTCATAGAGGCTCCCAAGAGTGTGGTGAAGTGGTGC 200  
QY 251 CCAGGCGGTGGGGCGCGTGAAGGCCCTGAAGGCCCTGCTGGGGCGCTGACAGTGTGTTG 310  
DB 199 CCAGGCGGTGGGGCGCGTGAAGGCCCTGAAGGCCCTGCTGGGGCGCTGACAGTGTGTTG 140  
QY 311 GC 312  
DB 139 GC 138

## RESULT 12

BI819045  
LOCUS 603033186F1 NIH\_MGC\_115 Homo sapiens cDNA clone IMAGE:5174540 5',  
DEFINITION mRNA sequence.

ACCESSION BI819045  
VERSION BI819045.1 GI:15930595  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
REFERENCE 1 (bases 1 to 961)  
AUTHORS Fukuyota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
TITLE Mammalia; Euthera; Primates; Catarrhini; Hominiidae; Homo.  
JOURNAL NIH-MGC <http://mgc.nci.nih.gov/>  
COMMENT Contact: Robert Strausberg, Ph.D.  
Unpublished (1999)  
Email: cgaps-r@mail.nih.gov  
Tissue Procurement: Life Technologies, Inc.  
cDNA Library Preparation: Life Technologies, Inc.  
DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
<http://image.llnl.gov>  
Plate: LLNL1434 row: k column: 21  
High quality sequence start: 3  
High quality sequence stop: 511.  
Location/Qualifiers  
1. .961  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
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/clone="IMAGE:5174540"

## FEATURES

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1. .961  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:5174540"

with a modified polylinker; Plasmid DNA from the  
normalized library NCI CGAP Pr22 was prepared, and ss  
circles were made in vitro. Following HAP purification,  
this DNA was used as tracer in a subtractive hybridization  
reaction. The driver was PCR-amplified cDNAs from a pool  
of 5,000 clones made from the same library (clonoids  
985608-986759, 1101192-1101959, and 1217928-1220615).  
Subtraction by Bento Soares and M. Fatima Bonaldo. "

/lab host="DH10B"  
 /clone lib="NIH\_MGC\_115"  
 /note="Organ: Pooled brain, lung, testis; Vector:  
 PCMV-SPORT6; Site 1: NotI; Site 2: EcoRV (destroyed); RNA  
 source anonymous pool of 6 male brains, age range 23-27; 1  
 male lung, age 27; and 1 male testis, age 69. Library is  
 oligo-dT primed and directionally cloned (EcoRV site is  
 destroyed upon cloning). Average insert size 1.8 kb,  
 insert size range 1-3 kb. Library is normalized and  
 enriched for full-length clones and was constructed by C.  
 Gruber (Invitrogen). Research Genetics tracking code  
 021. Note: this is a NIH\_MGC Library."

## ORIGIN

Query Match 95.4%; Score 297.8; DB 12; Length 961;  
 Best Local Similarity 99.0%; Pred. No. 2.1e-40;  
 Matches 310; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

QY 1 ATGAAGCTCGCC-GCCCTCCCTGGGGCTCTGGCTGGCCCTCTGCTCAGCTCCGCTCGTGC 59  
 Db 21 ATGAAGCTCGCGGCCCTCTGGGGCTCTGGCTGGCCCTCTGCTCAGCTCCGCTCGTGC 80

QY 60 TTCTTATTAGGGCTCGGCAAGCCCTGTGGCCAGCCTGTGCTGCTGCTGAGTGGCGGC 119  
 Db 81 TTCTTATTAGGGCTCGGCAAGCCCTGTGGCCAGCCTGTGCTGCTGAGTGGCGGC 140

QY 120 GGAGCGGGCGGCGGACCCCTGGCCAAACCCCTCGGACCCCTCAACCGCTGAAGCTCCT 179  
 Db 141 GGAGCGGGCGGCGGACCCCTGGCCAAACCCCTCGGACCCCTCAACCGCTGAAGCTCCT 200

QY 180 GCTGAGCAGCTGGGCATCCCGTGAACACCTCATAGAGGCTCCCGAGAGTGTGTGGC 239  
 Db 201 GCTGAGCAGCTGGGCATCCCGTGAACACCTCATAGAGGCTCCCGAGAGTGTGTGGC 260

QY 240 TGAGCTGGTCCCCAGGCGGTGGGGCGCGTGAAGCCCTGCTGCTGGGGCGCCCT 299  
 Db 261 TGAGCTGGTCCCCAGGCGGTGGGGCGCGTGAAGCCCTGCTGCTGGGGCGCCCT 320

QY 300 GACAGTGTGGC 312  
 Db 321 GACAGTGTGGC 333

RESULT 13  
 BI820788  
 LOCUS 603034390F1 NIH\_MGC\_115 Homo sapiens cDNA clone IMAGE:5175502 5',  
 mRNA sequence.  
 BI820788  
 DEFINITION 603034390F1 NIH\_MGC\_115 Homo sapiens cDNA clone IMAGE:5175502 5',  
 mRNA sequence.  
 ACCESSION BI820788.1 GI:15932338  
 VERSION EST.  
 KEYWORDS Homo sapiens (human)  
 SOURCE Homo sapiens  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 1 (bases 1 to 407)  
 NIH-MGC http://imgc.nci.nih.gov/  
 National Institutes of Health, Mammalian Gene Collection (MGC)  
 Unpublished (1999)  
 Contact: Robert Strausberg, Ph.D.  
 Email: cgabbs@mail.nih.gov  
 Tissue Procurement: Life Technologies, Inc.  
 cDNA Library Preparation: Life Technologies, Inc.  
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
 DNA Sequencing by: Incyte Genomics, Inc.  
 Clone Distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:  
 http://image.llnl.gov  
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 High quality sequence stop: 405.  
 Location/Qualifiers  
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## FEATURES

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 /clone lib="NIH\_MGC\_115"  
 /note="Organ: Pooled brain, lung, testis; Vector:  
 PCMV-SPORT6; Site 1: NotI; Site 2: EcoRV (destroyed); RNA  
 source anonymous pool of 6 male brains, age range 23-27; 1  
 male lung, age 27; and 1 male testis, age 69. Library is  
 oligo-dT primed and directionally cloned (EcoRV site is  
 destroyed upon cloning). Average insert size 1.8 kb,  
 insert size range 1-3 kb. Library is normalized and  
 enriched for full-length clones and was constructed by C.  
 Gruber (Invitrogen). Research Genetics tracking code  
 021. Note: this is a NIH\_MGC Library."

ORIGIN

Query Match 95.1%; Score 296.8; DB 12; Length 407;  
 Best Local Similarity 99.0%; Pred. No. 2.4e-40;  
 Matches 309; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

QY 1 ATGAAGCTCGCGCCCTCTGGGGCTCTGGCTGGCCCTCTGCTCAGCTCCGCTCGTGC 60  
 Db 8 ATGAAGCTCGCGCCCTCTGGGGCTCTGGCTGGCCCTCTGCTCAGCTCCGCTCGTGC 66

QY 61 TTCTTATTAGGGCTCGGCAAGCCCTGTGGCCAGCCTGTGCTGCTGAGTGGCGGC 120  
 Db 67 TTCTTATTAGGGCTCGGCAAGCCCTGTGGCCAGCCTGTGCTGCTGAGTGGCGGC 126

QY 121 GAGCGCGGGCGGCGGACCCCTGGCCAAACCCCTCGGACCCCTCAACCGCTGAAGCTCCTG 180  
 Db 127 GAGCGCGGGCGGCGGACCCCTGGCCAAACCCCTCGGACCCCTCAACCGCTGAAGCTCCTG 186

QY 181 CTGAGCAGCTGGGCATCCCGTGAACACCTCATAGAGGCTCCCGAGAGTGTGTGGCT 240  
 Db 187 CTGAGCAGCTGGGCATCCCGTGAACACCTCATAGAGGCTCCCGAGAGTGTGTGGCT 246

QY 241 GAGCTGGTCCCCAGGCGGTGGGGCGCGTGAAGCCCTGAGGCCCTCTGGGGCGCCCTG 300  
 Db 247 GAGCTGGTCCCCAGGCGGTGGGGCGCGTGAAGCCCTGAGGCCCTCTCTGGGGCGCCCTG 306

QY 301 ACAGTGTGGC 312  
 Db 307 ACAGTGTGGC 318

RESULT 14  
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 LOCUS 603032283T1 NIH\_MGC\_115 Homo sapiens cDNA clone IMAGE:5173268 3',  
 mRNA sequence.  
 BI490604  
 DEFINITION 603032283T1 NIH\_MGC\_115 Homo sapiens cDNA clone IMAGE:5173268 3',  
 mRNA sequence.  
 ACCESSION BI490604.1 GI:15329832  
 VERSION EST.  
 KEYWORDS Homo sapiens (human)  
 SOURCE Homo sapiens  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 1 (bases 1 to 416)  
 NIH-MGC http://imgc.nci.nih.gov/  
 National Institutes of Health, Mammalian Gene Collection (MGC)  
 Unpublished (1999)  
 Contact: Robert Strausberg, Ph.D.  
 Email: cgabbs@mail.nih.gov  
 Tissue Procurement: Life Technologies, Inc.  
 cDNA Library Preparation: Life Technologies, Inc.  
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
 DNA Sequencing by: Incyte Genomics, Inc.  
 Clone Distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:  
 http://image.llnl.gov  
 Plate: LLAM1431 row: f column: 21

High quality sequence start: 6  
High quality sequence stop: 416.  
Location/Qualifiers  
source  
1. 416

/organism="Homo sapiens"  
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/clone="IMAGE:5173268"  
/lab\_host="DH10B"  
/clone\_lib="NIH\_MGC\_115"  
/notes="Organ: pooled brain, lung, testis; Vector:  
pCMV-SPORT6; Site 1: NotI; Site 2: EcoRV (destroyed); RNA  
source anonymous pool of 6 male brains, age range 23-27; 1  
male lung, age 27; and 1 male testis, age 69. Library is  
oligo-dT primed and directionally cloned (EcoRV site is  
destroyed upon cloning). Average insert size 1.8 kb,  
insert size range 1-3 kb. Library is normalized and  
enriched for full-length clones and was constructed by C.  
Gruber (Invitrogen). Research Genetics tracking code  
021. Note: this is a NIH\_MGC Library."

## ORIGIN

Query Match 95.1%; Score 296.8; DB 12; Length 416;  
Best Local Similarity 99.0%; Pred. No. 2.5e-40;  
Matches 309; Conservative 0; Mismatches 2; Indels 1; Gaps 1;  
QY 1 ATGAAGCTGCGCCCTCTCGGGGCTGTGGTGGCCCTGTCGAGCTCCGTCGTGCT 60  
DB 393 ATGAAGCTGCGCCCTCTCGGGGCTGTGGTGGCCCTGTCGAGCTCCGTCGTGCT 334  
QY 61 TTCTTAGTGGGCTCGGCCAAGCCTGTGGCCAGCCCTGCTCGCTGGAGTCGGGGG 120  
DB 333 TTCTTAGTGGGCTCGGCCAAGCCTGTGGCCAGCCCTGCTCGCTGGAGTCGGGGG 274  
QY 121 GAGGCGGGGCGGGGACCCCTCGGCAACCCCTCGGCACCCCTCAACCCGCTGAAGCTCCTG 180  
DB 273 GAGGCGGGGCGGGGACCCCTCGGCAACCCCTCGGCACCCCTCAACCCGCTGAAGCTCCTG 215  
QY 181 CTGAGCAGCTGGGCAATCCCGTGAACACCTCATAGAGGCTCCAGAGTGTGGCT 240  
DB 214 CTGAGCAGCTGGGCAATCCCGTGAACACCTCATAGAGGCTCCAGAGTGTGGCT 155  
QY 241 GAGTGGTCCCCAGGCGCTGGGGCGGTGAAGCCCTGAAGCCCTGCTGGGGGCGCTG 300  
DB 154 GAGTGGTCCCCAGGCGCTGGGGCGGTGAAGCCCTGAAGCCCTGCTGGGGGCGCTG 95  
QY 301 ACAGTGTTTGGC 312  
DB 94 ACAGTGTTTGGC 83

## RESULT 15

BI819014  
LOCUS 491 bp mRNA linear EST 04-OCT-2001  
DEFINITION 603033130F1 NIH\_MGC\_115 Homo sapiens cDNA clone IMAGE:5174526 5',  
mRNA sequence.

ACCESSION BI819014  
VERSION BI819014.1 GI:15930564

KEYWORDS EST.

SOURCE Homo sapiens (human)

## ORGANISM

Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 491)

NIH-MGC <http://mgc.nci.nih.gov/>.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: [cgapsb@mail.nih.gov](mailto:cgapsb@mail.nih.gov)

Tissue Procurement: Life Technologies, Inc.

cDNA Library Preparation: Life Technologies, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
<http://image.llnl.gov>  
Plate: LLAM11434 row: k column: 07  
High quality sequence stop: 470.  
Location/Qualifiers  
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1. 491

/organism="Homo sapiens"  
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/clone="IMAGE:5174526"  
/lab\_host="DH10B"  
/clone\_lib="NIH\_MGC\_115"  
/notes="Organ: pooled brain, lung, testis; Vector:  
pCMV-SPORT6; Site 1: NotI; Site 2: EcoRV (destroyed); RNA  
source anonymous pool of 6 male brains, age range 23-27; 1  
male lung, age 27; and 1 male testis, age 69. Library is  
oligo-dT primed and directionally cloned (EcoRV site is  
destroyed upon cloning). Average insert size 1.8 kb,  
insert size range 1-3 kb. Library is normalized and  
enriched for full-length clones and was constructed by C.  
Gruber (Invitrogen). Research Genetics tracking code  
021. Note: this is a NIH\_MGC Library."

## ORIGIN

Query Match 95.1%; Score 296.8; DB 12; Length 491;  
Best Local Similarity 99.0%; Pred. No. 2.6e-40;  
Matches 309; Conservative 0; Mismatches 2; Indels 1; Gaps 1;  
QY 1 ATGAAGCTGCGCCCTCTCGGGGCTGTGGTGGCCCTGTCGAGCTCCGTCGTGCT 60  
DB 22 ATGAAGCTGCGCG-CCTCCTGGGGCTGTGGTGGCCCTGTCGAGCTCCGTCGTGCT 80  
QY 61 TTCTTAGTGGGCTCGGCCAAGCCTGTGGCCAGCCCTGCTCGCTGGAGTCGGGGG 120  
DB 81 TTCTTAGTGGGCTCGGCCAAGCCTGTGGCCAGCCCTGCTCGCTGGAGTCGGGGG 140  
QY 121 GAGGCGGGGCGGGGACCCCTCGGCAACCCCTCGGCAACCCCTCAACCCGCTGAAGCTCCTG 180  
DB 141 GAGGCGGGGCGGGGACCCCTCGGCAACCCCTCGGCAACCCCTCAACCCGCTGAAGCTCCTG 200  
QY 181 CTGAGCAGCTGGGCATCCCGTGAACACCTCATAGAGGCTCCAGAGTGTGGCT 240  
DB 201 CTGAGCAGCTGGGCATCCCGTGAACACCTCATAGAGGCTCCAGAGTGTGGCT 260  
QY 241 GAGTGGTCCCCAGGCGCTGGGGCGGTGAAGCCCTGAAGCCCTGCTGGGGGCGCTG 300  
DB 261 GAGTGGTCCCCAGGCGCTGGGGCGGTGAAGCCCTGAAGCCCTGCTGGGGGCGCTG 320  
QY 301 ACAGTGTTTGGC 312  
DB 321 ACAGTGTTTGGC 332

Search completed: June 6, 2004, 15:41:35

Job time : 2503 secs

1	56.4	18.1	263	2	US-08-964-725-2	Sequence 2, Appli
2	56.4	18.1	507	2	US-08-964-725-2	Sequence 4, Appli
3	56.4	18.1	519	2	US-08-964-725-4	Sequence 5, Appli
4	52.4	16.8	509	4	US-09-023-655-267	Sequence 267, App
5	49.2	15.8	2497	4	US-09-620-312D-47	Sequence 47, Appl
6	46.6	14.9	2274	4	US-09-252-931A-3660	Sequence 3660, Ap
7	46.6	14.9	3297	4	US-09-252-931A-3615	Sequence 3615, Ap
8	46.2	14.8	432	4	US-09-252-931A-13281	Sequence 13281, A
9	46.2	14.8	1425	4	US-09-252-931A-12820	Sequence 12820, A
10	46.2	14.8	1428	4	US-09-252-931A-12677	Sequence 12677, A
11	46.2	14.8	1611	4	US-09-252-931A-13122	Sequence 13122, A
12	44.2	14.2	729	4	US-09-252-931A-7316	Sequence 7316, Ap
13	44.2	14.2	1083	4	US-09-252-931A-7185	Sequence 7185, Ap
14	44.2	14.2	1572	4	US-09-252-931A-7304	Sequence 7304, Ap
15	44.2	14.2	2543	1	US-08-555-669-11	Sequence 11, Appl
16	44.2	14.2	2543	3	US-09-073-663-11	Sequence 11, Appl
17	44.2	14.2	2574	4	US-09-252-931A-7385	Sequence 7385, Ap
18	43.6	14.0	432	1	US-08-642-255-48	Sequence 48, Appl
19	43.6	14.0	7751	1	US-08-642-255-50	Sequence 50, Appl
20	42.6	13.7	2721	6	5215891-2	Patent No. 5215891
21	42.6	13.7	8438	1	US-07-945-283-1	Sequence 1, Appli
22	42.2	13.5	930	4	US-09-252-931A-1173	Sequence 1173, Ap
23	42.2	13.5	1116	4	US-09-252-931A-8238	Sequence 8238, Ap
24	42.2	13.5	1122	4	US-09-252-931A-7974	Sequence 7974, Ap
25	42.2	13.5	1125	4	US-09-252-931A-8074	Sequence 8074, Ap
26	42.2	13.5	1936	4	US-09-475-515-47	Sequence 47, Appl
27	42.2	13.5	1944	4	US-09-475-515-37	Sequence 37, Appl



US-08-964-725-2

Query Match 18.1%; Score 56.4; DB 2; Length 263;  
Best Local Similarity 60.4%; Pred. No. 0.0013;  
Matches 93; Conservative 0; Mismatches 61; Indels 0; Gaps 0;

QY 137 CCTGGCCAAACCCCTCGGACCCCTCAACCGCTGAAGCTCCTGCTGAGCAGCCTGGGCA 196  
DB 60 CTCGGACAACAATCTCCCTTTAAGATCCATTAAAGCTTCTTCTGAAGAACTCTGGGCA 119  
QY 197 TCCCGGTGAACCACTCATAGAGGGCTCCACAGAGTGTGTGGCTGAGCTGGGTCCCGCAGG 256  
DB 120 TTTCTGTGTGAGCACCTTGTGGAGGGCTAAGGAAGTGTGTAATGAGCTGGGACCAAGG 179  
QY 257 CCGTGGGGGGCGGTGAAGCCCTGAAGGCCCTGCT 290  
DB 180 CTTCTGAAGCTGTGAAGAACTGCTGGAGGCGCT 213

## RESULT 2

US-08-964-725-4  
; Sequence 4, Application US/08964725  
; Patent No. 5939265

## GENERAL INFORMATION:

; APPLICANT: COHEN, Maurice  
; APPLICANT: FRIEDMAN, Paula N.  
; APPLICANT: GORDON, Julian  
; APPLICANT: HODGES, Steven C.  
; APPLICANT: KLASS, Michael R.  
; APPLICANT: KRATOCHVIL, Jon D.  
; APPLICANT: ROBERTS-RAPP, Lisa  
; APPLICANT: RUSSELL, John C.  
; APPLICANT: STROUPE, Steven D.

; TITLE OF INVENTION: REAGENTS AND METHODS USEFUL

; TITLE OF INVENTION: FOR DETECTING DISEASES OF THE LUNG

; NUMBER OF SEQUENCES: 19

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Abbott Laboratories  
; STREET: 100 Abbott Park Road  
; CITY: Abbott Park  
; STATE: IL

; COUNTRY: USA

; ZIP: 60064-3500

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: DOS

; SOFTWARE: FastSeq for Windows Version 2.0

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/964,725

; FILING DATE:

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER:

; FILING DATE:

; ATTORNEY/AGENT INFORMATION:

; NAME: Becker, Cheryl L.

; REGISTRATION NUMBER: 35,441

; REFERENCE/DOCKET NUMBER: 5997.US.P1

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 847/935-1729

; TELEFAX: 847/938-2623

; TELEX:

; INFORMATION FOR SEQ ID NO: 4:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 507 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

US-08-964-725-4

Query Match 18.1%; Score 56.4; DB 2; Length 507;  
Best Local Similarity 60.4%; Pred. No. 0.0014;

Matches 93; Conservative 0; Mismatches 61; Indels 0; Gaps 0;

QY 137 CCTGGCCAAACCCCTCGGACCCCTCAACCGCTGAAGCTCCTGCTGAGCAGCCTGGGCA 196  
DB 195 CTCGGACAACAATCTCTCCCTTTATGATCCATTAAAGCTTCTTCTGAAGAACTCTGGGCA 254  
QY 197 TCCCGGTGAACCACTCATAGAGGGCTCCACAGAGTGTGTGGCTGAGCTGGGTCCCGCAGG 256  
DB 255 TTTCTGTGTGAGCACCTTGTGGAGGGCTAAGGAAGTGTGTAATGAGCTGGGACCAAGG 314  
QY 257 CCGTGGGGGGCGGTGAAGCCCTGAAGGCCCTGCT 290  
DB 315 CTTCTGAAGCTGTGAAGAACTGCTGGAGGCGCT 348

## RESULT 3

US-08-964-725-5  
; Sequence 5, Application US/08964725  
; Patent No. 5939265

## GENERAL INFORMATION:

; APPLICANT: COHEN, Maurice  
; APPLICANT: FRIEDMAN, Paula N.  
; APPLICANT: GORDON, Julian  
; APPLICANT: HODGES, Steven C.  
; APPLICANT: KLASS, Michael R.  
; APPLICANT: KRATOCHVIL, Jon D.  
; APPLICANT: ROBERTS-RAPP, Lisa  
; APPLICANT: RUSSELL, John C.  
; APPLICANT: STROUPE, Steven D.  
; TITLE OF INVENTION: REAGENTS AND METHODS USEFUL  
; TITLE OF INVENTION: FOR DETECTING DISEASES OF THE LUNG  
; NUMBER OF SEQUENCES: 19  
; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Abbott Laboratories

; STREET: 100 Abbott Park Road

; CITY: Abbott Park

; STATE: IL

; COUNTRY: USA

; ZIP: 60064-3500

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: DOS

; SOFTWARE: FastSeq for Windows Version 2.0

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/964,725

; FILING DATE:

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER:

; FILING DATE:

; ATTORNEY/AGENT INFORMATION:

; NAME: Becker, Cheryl L.

; REGISTRATION NUMBER: 35,441

; REFERENCE/DOCKET NUMBER: 5997.US.P1

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 847/935-1729

; TELEFAX: 847/938-2623

; TELEX:

; INFORMATION FOR SEQ ID NO: 5:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 519 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

US-08-964-725-5

Query Match 18.1%; Score 56.4; DB 2; Length 519;  
Best Local Similarity 60.4%; Pred. No. 0.0014;

Matches 93; Conservative 0; Mismatches 61; Indels 0; Gaps 0;

QY 137 CCTGGCCAAACCCCTCGGACCCCTCAACCGCTGAAGCTCCTGCTGAGCAGCCTGGGCA 196  
DB 195 CTCGGACAACAATCTCTCCCTTTATGATCCATTAAAGCTTCTTCTGAAGAACTCTGGGCA 254  
QY 197 TCCCGGTGAACCACTCATAGAGGGCTCCACAGAGTGTGTGGCTGAGCTGGGTCCCGCAGG 256  
DB 255 TTTCTGTGTGAGCACCTTGTGGAGGGCTAAGGAAGTGTGTAATGAGCTGGGACCAAGG 314

Db 208 CTCTGACAAACATCTCCCTTTATGATCCATTAAAGCTTCTTCTGAAACATCTGGGCA 267  
QY 197 TCCCGCTGAACACCTCATAGAGGGCTCCAGAGTGCTGGCTAGCTGGGTCCCGAG 256  
Db 268 TTTCGTTGAGCACCTTGTTGGAGGGCTAAGAGTGTTGTAATAGCTGGGACCGAGG 327  
QY 257 CGGTGGGGCCGTGAAGGCCCTTGAAGGCCCTGCT 290  
Db 328 CTTCTGAAGCTGGAAGAACTGCTGGAGGCGCT 361

RESULT 4  
US-09-023-655-267  
; Sequence 267, Application US/09023655  
; Patent No. 6607879  
; GENERAL INFORMATION:  
; APPLICANT: Cocks, Benjamin G.  
; APPLICANT: Susan G. Stuart  
; APPLICANT: Jeffrey J. Seilhamer  
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE  
; TITLE OF INVENTION: EXPRESSION  
; NUMBER OF SEQUENCES: 1508  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.  
; STREET: 3174 PORTER DRIVE  
; CITY: PALO ALTO  
; STATE: CALIFORNIA  
; COUNTRY: USA  
; ZIP: 94304  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/023,655  
; FILING DATE: HEREWITH  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; CLASSIFICATION:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Zeller, Karen J.  
; REGISTRATION NUMBER: 37,071  
; REFERENCE/DOCKET NUMBER: PA-0001 US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (650) 855-0555  
; TELEFAX: (650) 845-4166  
; INFORMATION FOR SEQ ID NO: 267:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 509 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; IMMEDIATE SOURCE:  
; LIBRARY: LUNGNOT01  
; CLONE: 126758  
US-09-023-655-267

Query Match 16.8%; Score 52.4; DB 4; Length 509;  
Best Local Similarity 59.3%; Pred. No. 0.0092;  
Matches 89; Conservative 0; Mismatches 61; Indels 0; Gaps 0;

QY 141 GCGCAACCCCTCGGCACCTCAACCGCTGAAGCTCTCTGAGCAGCGTGGGATCCC 200  
Db 201 GACAAACATCTCTCCCTTTATGGATCCATTAAAGCTTCTTCTGAAACATCTGGGCAATTTC 260  
QY 201 CGTGAACACCTCATAGAGGCTCCAGAGTGCTGGCTGAGCTGGGTCGCCAGGCCCT 260  
Db 261 TGTGAGCACCTTGTGGAGGGGCTAAGAGTGTTGTAATAGCTGGGACCGAGGCTTC 320  
QY 261 GGGGGCGTGAAGGCCCTGAAGGCCCTGCT 290

Db 321 TGAAGCTGTGAAGAACTGCTGGAGGCGCT 350

RESULT 5  
US-09-620-312D-47  
; Sequence 47, Application US/09620312D  
; Patent No. 6569662  
; GENERAL INFORMATION:  
; APPLICANT: Tang, Y. Tom  
; APPLICANT: Liu, Chinghua  
; APPLICANT: Asundi, Vinod  
; APPLICANT: Zhang, Jie  
; APPLICANT: Ren, Feiyan  
; APPLICANT: Chen, Rui-hong  
; APPLICANT: Zhao, Qing A.  
; APPLICANT: Wehrman, Tom  
; APPLICANT: Xue, Aidong J.  
; APPLICANT: Wang, Yonghong  
; APPLICANT: Wang, Jian-Rui  
; APPLICANT: Zhou, Ping  
; APPLICANT: Ma, Yunqing  
; APPLICANT: Wang, Dunrui  
; APPLICANT: Wang, Zhiwei  
; APPLICANT: John Tillinghast  
; APPLICANT: Drmanac, Radoje T.  
; TITLE OF INVENTION: No. 6569662el Nucleic Acids and  
; TITLE OF INVENTION: Polypeptides  
; FILE REFERENCE: 784CIP2B  
; CURRENT APPLICATION NUMBER: US/09/620,312D  
; CURRENT FILING DATE: 2000-07-19  
; PRIOR APPLICATION NUMBER: 09/552,317  
; PRIOR FILING DATE: 2000-04-25  
; PRIOR APPLICATION NUMBER: 09/488,725  
; PRIOR FILING DATE: 2000-01-21  
; NUMBER OF SEQ ID NOS: 1105  
; SOFTWARE: pt\_FL\_genes Version 1.0  
; SEQ ID NO 47  
; LENGTH: 2497  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (107)..(1756)  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: (1)...(2497)  
; OTHER INFORMATION: n = a,t,c or g  
US-09-620-312D-47

Query Match 15.8%; Score 49.2; DB 4; Length 2497;  
Best Local Similarity 50.0%; Pred. No. 0.045;  
Matches 151; Conservative 0; Mismatches 148; Indels 3; Gaps 1;

QY 3 GAAGCTCGCGCCCTCTCGGGCTCTGGCTGGCCCTGTGCTGAGCTCGGCTCGGTGCTTT 62  
Db 1099 GTACCTGGTCCCTGAGCGCGGCTGAGGAGGCTTGGGACAGAGTCCCTCGCGGCTT 1158  
QY 63 CTTAGTGGGCTG---GCCAAGCTGTGGCCAGCCTGTGCTGGCTGGAGTGGGCGGC 119  
Db 1159 CGTGGGGAGGTGGGTGCGCCGCTCTGCGGCGCCCGGGGGCGGCTCGTGGGCGGCGC 1218  
QY 120 GGAGCGCGGCGGAGCCCTGGCCAAACCCCTCGGACCCCTCAACCGCTGAAGCTCCT 179  
Db 1219 TCGGCCATGGTGGCGGCTGGGCTCCATGGTGGGCTCATGACCTACGGGCGGCGCA 1278  
QY 180 GCTGAGCAGCTTGGGCATCCCGTGAACCACTCATAGAGGCTCCCAAGAGTGTGGC 239  
Db 1279 ATTCCAGTCCCTGGACAGCATGGGCGGCTGATCCCGCCCTTCCGAGGCTTCGCG 1338  
QY 240 TGAGCTGGTCCCGAGGCGGTGGGGCGCGTGAAGGCCCTGAAGGCCCTGTGGGGCGCT 299  
Db 1339 CAAGCTAACCAAGCTGTGGATGCCAGCGCGGAGGCTTTCACCGCTTACCTGGAAGCAAT 1398

```
QY 300 GA 301
Db 1399 GA 1400

Matches 109; Conservative 0; Mismatches 104; Indels 0; Gaps 0;

88 GCCAGCCTGTCCTGGCTGAGTGGCGGCGAGGCGCGGACCTTGGCCAC 147
161 GTCTGTGTTCCGCGCGCAGCGCTCGCGCGGAGATCGCACCCGATAC 220
148 CCCTCGGCACCTCAACCGCTGAAGCTCTCTGAGCAGCTGGGCATCCCGTGAAC 207
221 TACGGCTGCCCGCAGCGCTGGAGAGCGCTGAACACCTAGCCCGCAGCGCGC 280
208 CACCTCATAGAGGCTCCCAAGAGTGTGTGGCTGAGCTGGGTCCCGAGCGGTGGGGGCC 267
281 GTGTGATCCCTTCAGCCCGGACAGACCGCGCGCGGCGAGCCAGCGGTGGACGGC 340
268 GTGAAGGCCCTGAAGCCCTGTGGGGCCCTG 300
341 GAGTACACCTGGAGGAAGCCCTGGCGGCCCTG 373

Db

RESULT 8
US-09-252-991A-13281/c
; Sequence 13281, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 13281
; LENGTH: 432
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-13281

Query Match 14.8%; Score 46.2; DB 4; Length 432;
Best Local Similarity 47.2%; Pred. No. 0.18;
Matches 141; Conservative 0; Mismatches 158; Indels 0; Gaps 0;

QY 9 CGCGCCCTCTCTGGGCTCTGGTGGCCCTGTCTGCAGCTCGCTCGTCTTCTAGT 68
Db 408 CGCGGTGGCACCGGGCTCAACGCGCGGAGGCTTCGCGAGCCCATCCCGGGAAT 349
69 GGGCTCGGCCAACGCTGTGGCCAGCCTGTCTGCCTGAGTTCGGCGGAGGCGCGG 128
348 CGCGCGGATCGGGCTGTCTTCGTCGCGCGGCGAACAGTTCGCCGCCCTGGCGG 289
129 GGCGGGACCTTGGCCAAACCCCTCGGCAACCTCAACCCCGCTGAAGCTCTGTGAGCAG 188
288 CCAGAGCGCTGTGTATCTCTCGCGCGCTCAAGAGCTCGCGGTGCGCTGATGAA 229
189 CTTGGGATCCCGTGAACCACTCATAGAGGCTCCAGAGTGTGTGCTGAGCTGGG 248
228 GATGCCAACAGACTTGCCTGTCTCGGTCGCGCGCGGCTTCGCCCGAGGTGAA 169
249 TCCCGAGCGCTGGGGCGCGTGAAGGCCCTGAAGGCCCTGTGGGGCCCTGACAGTGT 307
168 GCTCCGGCCAAAGAGCGCGGCGCTCGATCATGTCGCCGGAAGTCAACCGCAGT 110

Db

RESULT 9
US-09-252-991A-12820
; Sequence 12820, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
```

;; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

;; FILE REFERENCE: 107196.136  
;; CURRENT APPLICATION NUMBER: US/09/252,991A  
;; CURRENT FILING DATE: 1999-02-18  
;; PRIOR APPLICATION NUMBER: US 60/074,788  
;; PRIOR FILING DATE: 1998-02-18  
;; PRIOR APPLICATION NUMBER: US 60/094,190  
;; PRIOR FILING DATE: 1998-07-27  
;; NUMBER OF SEQ ID NOS: 33142  
;; SEQ ID NO 12820  
;; LENGTH: 1425  
;; TYPE: DNA  
;; ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-12820

Query Match 14.8%; Score 46.2; DB 4; Length 1425;  
Best Local Similarity 47.2%; Pred. No. 0.18; Mismatches 158; Indels 0; Gaps 0;  
Matches 141; Conservative 0;

QY 9 CGCCGCGCTCTCGTGGGCTCTGGTGGCCCTGCTCTGAGCTCGGCTCGTCTTCTTAGT 68  
DB 714 CGCGGTGGCCACCGGGCTCAACGGCGCGAAGGCTTCGCCGAGCCATCGCCGCGGAAT 773  
QY 69 GGGCTCGCCCAAGCCTGTGGCCAGCCTGTGCTGGCTGGAGTGGCGGGGAGGCCGG 128  
DB 774 CGCCGCGGAATCGGGCTCGCTTCTGTCGCCGCGCGCAAGTTCCGCCGCCCTGGCCGG 833  
QY 129 GCGCGGACCTGGCAACCCCTCGGACCTCAACCCGCTGAAGCTCCTCTGAGCAG 188  
DB 834 CACGAGCGCTGGTTCATCTCTCCGCGGCTTGAAGCGCTGGCGGCTGATGAA 893  
QY 189 CCTGGGCATCCCGTGAACCACTCATAGAGGCTCCAGAGTGTGTGGCTGAGCTGG 248  
DB 894 GATGCCAAGACCTCGCTGCTCGGTTCCGCCCAACCGCGGCTTCGCCGAGTGAA 953  
QY 249 TCCCGAGCGGTGGGGCGGTGAAGCCCTGAAGCCCTGCTGGGGGCGCTGACAGTGT 307  
DB 954 GCTGCGCGCAACGAGCGCGGAGCTCGATCATGTCGCCGCAAGGTCAACCCGACCCAGT 1012

RESULT 10  
US-09-252-991A-12677  
;; Sequence 12677, Application US/09252991A  
;; Patent No. 6551795  
;; GENERAL INFORMATION:  
;; APPLICANT: Marc J. Rubenfield et al.  
;; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
;; FILE REFERENCE: 107196.136  
;; CURRENT APPLICATION NUMBER: US/09/252,991A  
;; CURRENT FILING DATE: 1999-02-18  
;; PRIOR APPLICATION NUMBER: US 60/074,788  
;; PRIOR FILING DATE: 1998-02-18  
;; PRIOR APPLICATION NUMBER: US 60/094,190  
;; PRIOR FILING DATE: 1998-07-27  
;; NUMBER OF SEQ ID NOS: 33142  
;; SEQ ID NO 12677  
;; LENGTH: 1428  
;; TYPE: DNA  
;; ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-12677

Query Match 14.8%; Score 46.2; DB 4; Length 1428;  
Best Local Similarity 47.2%; Pred. No. 0.18;  
Matches 141; Conservative 0; Mismatches 158; Indels 0; Gaps 0;

QY 9 CGCCGCGCTCTCGTGGGCTCTGGTGGCCCTGCTCTGAGCTCGGCTCGTCTTCTTAGT 68  
DB 661 CGCGGTGGCCACCGGGCTCAACGGCGCGAAGGCTTCGCCGAGCCATCGCCGCGGAAT 720  
QY 69 GGGCTCGCCCAAGCCTGTGGCCAGCCTGTGCTGGCTGGAGTGGCGGGGAGGCCGG 128  
DB 721 CGCCGCGGAATCGGGCTCGCTTCTGTCGCCGCGCGCAAGTTCCGCCGCCCTGGCCGG 780

QY 129 GCGCGGACCTCGTGGGCGGTGAAGCCCTCAAGCCCTGAAGCTCCTCTGAGCAG 188  
DB 781 CCACGAGCGGTGGTTCATCTCTCGCGGCGCTGAAGAGCCCTGGCGCTGATGAA 840  
QY 189 CTTGGGATCCCGTGAACCACTCATAGAGGCTCCAGAAAGTGTGTGGCTGAGCTGG 248  
DB 841 GATCGCCCAACGACCTTGGCTGCTCGGTTCCGGGCCACGCGCGCTTCGCCGAGGTGAA 900  
QY 249 TCCCGAGCGGTGGGGCGGTGAAGCCCTGAAGCCCTGCTGGGGGCGCTGACAGTGT 307  
DB 901 GCTGCGCGCAACGAGCGCGGCGAGCTCGATCATGTCGCCGCAAGGTCAACCCGACCCAGT 959

RESULT 11  
US-09-252-991A-13122/c  
;; Sequence 13122, Application US/09252991A  
;; Patent No. 6551795  
;; GENERAL INFORMATION:  
;; APPLICANT: Marc J. Rubenfield et al.  
;; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
;; FILE REFERENCE: 107196.136  
;; CURRENT APPLICATION NUMBER: US/09/252,991A  
;; CURRENT FILING DATE: 1999-02-18  
;; PRIOR APPLICATION NUMBER: US 60/074,788  
;; PRIOR FILING DATE: 1998-02-18  
;; PRIOR APPLICATION NUMBER: US 60/094,190  
;; PRIOR FILING DATE: 1998-07-27  
;; NUMBER OF SEQ ID NOS: 33142  
;; SEQ ID NO 13122  
;; LENGTH: 1611  
;; TYPE: DNA  
;; ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-13122

Query Match 14.8%; Score 46.2; DB 4; Length 1611;  
Best Local Similarity 47.2%; Pred. No. 0.19; Mismatches 158; Indels 0; Gaps 0;  
Matches 141; Conservative 0;

QY 9 CGCCGCGCTCTCGTGGGCTCTGGTGGCCCTGCTCTGAGCTCGGCTCGTCTTCTTAGT 68  
DB 817 CGCGGTGGCCACCGGGCTCAACGGCGCGAAGGCTTCGCCGAGCCATCGCCGCGGAAT 758  
QY 69 GGGCTCGCGCAAGCCTGTGGCCAGCCTGTCTGCTGCTGAGTGGCGGGGAGGCCGG 128  
DB 757 CGCCGCGGATCGGGCTCGCTTCTGTCGCCGCGCGAACAAGTTTCGCCGCCCTGGCCGG 698  
QY 129 GCGCGGACCTCGGCGCAACCCCTCGGCAACCTCAACCCGCTGAAGCTCCTGCTGAGCAG 188  
DB 697 CCACGAGCGGTGGTTCATCTCTCGCGGCGCTTGAAGAGCTGGCGCTGATGAA 638  
QY 189 CTTGGGATCCCGTGAACCACTCATAGAGGCTCCAGAAAGTGTGTGGCTGAGCTGG 248  
DB 637 GATCGCCCAACGACCTTGGCTGCTCGGTTCCGGGCCACGCGCGCTTCGCCGAGGTGAA 578  
QY 249 TCCCGAGCGGTGGGGCGGTGAAGCCCTGGAAGCCCTGCTGGGGGCGCTGACAGTGT 307  
DB 577 GCTGCGCGCAACGAGCGCGGCGAGCTCGATCATGTCGCCGCAAGGTCAACCCGACCCAGT 519

RESULT 12  
US-09-252-991A-7316  
;; Sequence 7316, Application US/09252991A  
;; Patent No. 6551795  
;; GENERAL INFORMATION:  
;; APPLICANT: Marc J. Rubenfield et al.  
;; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
;; FILE REFERENCE: 107196.136  
;; CURRENT APPLICATION NUMBER: US/09/252,991A  
;; CURRENT FILING DATE: 1999-02-18  
;; PRIOR APPLICATION NUMBER: US 60/074,788



MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA: US/08/555.669  
APPLICATION NUMBER: US/08/555.669  
FILING DATE: 13-NOV-1995  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Halluin, Albert P.  
REGISTRATION NUMBER: 25,227  
REFERENCE/DOCKET NUMBER: 8389-030  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-854-3660  
TELEFAX: 415-854-3694  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 11:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2543 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: unknown  
TOPOLOGY: unknown  
MOLECULE TYPE: cDNA  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 47..2098  
US-08-555-669-11

Query Match 14.2%; Score 44.2; DB 1; Length 2543;  
Best Local Similarity 47.3%; Pred. No. 0.49;  
Matches 133; Conservative 0; Mismatches 148; Indels 0; Gaps 0;  
QY 6 GCTCGCGCCCTCTCTGGGGTCTCGCTGGCCCTGCTCTGCGAGCTCCGCTGCTTTCTT 65  
Db 1211 GCCCTCGGCCACAGGCCCTCCCGAGCCCTCGGTCTCGAGGCTTCAGGGCCAGAAG 1270  
QY 66 AGTGGGCTCGGCCAAGCCTGTGGCCCAAGCCTGTGCTGGCTGGAGTCGGCGCGAGGC 125  
Db 1271 GGCAGCATGGAGACCCCGGCTTCCAGGGCCCGAGGCTCCGAGGTGAGTGGGCGAC 1330  
QY 126 CGGGGCGGACCTGGCCACCCCTCGGACCCCTCAACCCGCTGAAGCTCTGCTGAG 185  
Db 1331 CGGGGCTCGGAGGTGCCGAAGGCCCTAAGGGAGACCAGGGTATTGAGGTTCCGACGGT 1390  
QY 186 CAGCCTGGGCATCCCGCTGAACCACTCATAGAGGGCTCCAGAGTGTGTGCTGAGCT 245  
Db 1391 CTTCTGGGATTAAGAGACTGGGTCCCGAGGCTTGGTGGACCCCAAGAGAGTCT 1450  
QY 246 GGGTCCCGAGCCGTGGGGCCGCTGAAGCCCTGAAGGCC 286  
Db 1451 GGCAGTCGAGGGAGCTGGGCCCCCAAGGACCCAGGGTCC 1491

Search completed: June 6, 2004, 15:43:07  
Job time : 81 secs



QY 121 GAGCGCGGGCGGACCCCTGGGCAACCCCTCGGCAACCCCTCAACCCGCTGAAGCTCTG 180  
Db 121 GAGCGCGGGCGGACCCCTGGGCAACCCCTCGGCAACCCCTCAACCCGCTGAAGCTCTG 180  
QY 181 CTGAGCAGCCTGGGCAATCCCTGGAACCACTCATAGAGGCTCCCAAGAGTGTGGCT 240  
Db 181 CTGAGCAGCCTGGGCAATCCCTGGAACCACTCATAGAGGCTCCCAAGAGTGTGGCT 240  
QY 241 GAGCTGGGTCCCAAGGCGTGGGGCGTGAAGCCCTGAAGGCCCTGCTGGGGGCCCTG 300  
Db 241 GAGCTGGGTCCCAAGGCGTGGGGCGTGAAGGCCCTGCTGGGGGCCCTG 300  
QY 301 ACAGTGTGTCG 312  
Db 301 ACAGTGTGTCG 312

## RESULT 2

US-10-426-002-18

; Sequence 18, Application US/10426002

; Publication No. US20040101876A1

; GENERAL INFORMATION:

; APPLICANT: Mintz, Liat

; APPLICANT: Xie, Hanging

; APPLICANT: Dahari, Dvir

; APPLICANT: Levanon, Erez

; APPLICANT: Freilich, Shiri

; APPLICANT: Beck, Nili

; APPLICANT: Zhu, Wei-yong

; APPLICANT: Wasserman, Alon

; APPLICANT: Hermesh, Chen

; APPLICANT: Azar, Idit

; APPLICANT: Bernstein, Jeanne

; APPLICANT: Rotem Sorek

; TITLE OF INVENTION: METHODS AND SYSTEMS USEFUL FOR ANNOTATING BIOMOLECULAR SEQUENCES

; FILE REFERENCE: 26083

; CURRENT APPLICATION NUMBER: US/10/426,002

; CURRENT FILING DATE: 2003-04-30

; NUMBER OF SEQ ID NOS: 41

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 18

; LENGTH: 527

; TYPE: DNA

; ORGANISM: Homo sapiens

US-10-426-002-18

Query Match 99.0%; Score 308.8; DB 17; Length 527;  
Best Local Similarity 99.4%; Pred. No. 4.7e-67;  
Matches 310; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ATGAAGCTCGCGCCCTCTCTGGGGCTCTCGTGGGCTCTGCGTGGCCCTGTCTGCAGCTCCGCTCGTCT 60  
Db 88 ATGAAGCTCGCGCCCTCTCTGGGGCTCTGCGTGGGCTCTGCGTGGCCCTGTCTGCAGCTCGTCTCT 147  
QY 61 TTCTTAGTGGGCTCGGCCAAGCCTCTGGCCCAAGCCTGTGCTGGTGGCTGAGTTCGGCGCG 120  
Db 148 TTCTTAGTGGGCTCGGCCAAGCCTCTGGCCCAAGCCTGTGCTGGTGGCTGAGTTCGGCGCG 207  
QY 121 GAGCGCGGGCGGAGCCTGTGCGCAACCCCTCGGACACCTCAACCCGCTGAAGTCTCTG 180  
Db 208 GAGCGCGGGCGGAGCCTGTGCGCAACCCCTCGGACACCTCAACCCGCTGAAGTCTCTG 267  
QY 181 CTGAGCAGCCTGGGATCCCTGTGAACCACTCATAGAGGGTCCCAAGAGTGTGCT 240  
Db 268 CTGAGCAGCCTGGGATCCCTGTGAACCACTCATAGAGGGTCCCAAGAGTGTGCT 327  
QY 241 GAGCTGGGTCCCAAGGCGTGGGGCGTGAAGGCCCTGAAGGCCCTGCTGGGGGCCCTG 300  
Db 328 GAGCTGGGTCCCAAGGCGTGGGGCGTGAAGGCCCTGAAGGCCCTGCTGGGGGCCCTG 387  
QY 301 ACAGTGTGTCG 312  
Db 388 ACAGTGTGTCG 399

## RESULT 3

US-10-237-435-6

; Sequence 6, Application US/10237435

; Publication No. US20030124580A1

; GENERAL INFORMATION:

; APPLICANT: Walker, Michael G.

; APPLICANT: Spiro, Peter A.

; APPLICANT: Marry, Lynn E.

; TITLE OF INVENTION: LUNG SURFACTANT MOLECULES

; FILE REFERENCE: PB-0019 US

; CURRENT APPLICATION NUMBER: US/10/237,435

; CURRENT FILING DATE: 2002-09-06

; PRIOR APPLICATION NUMBER: 60/317,822

; PRIOR FILING DATE: 09-07-2001

; NUMBER OF SEQ ID NOS: 9

; SOFTWARE: PERL Program

; SEQ ID NO 6

; LENGTH: 561

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: misc feature

; OTHER INFORMATION: Incyte ID No. US20030124580A1 242745.1

US-10-237-435-6

Query Match 99.0%; Score 308.8; DB 15; Length 561;  
Best Local Similarity 99.4%; Pred. No. 4.6e-67;  
Matches 310; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ATGAAGCTCGCGCCCTCTCTGGGGCTCTGCGTGGCCCTGTCTGCAGCTCCGCTCGTCTGCT 60  
Db 117 ATGAAGCTCGCGCCCTCTCTGGGGCTCTGCGTGGCCCTGTCTGCAGCTCCGCTCGTCTGCT 176  
QY 61 TTCTTAGTGGGCTCGGCCAAGCCTGTGCGCCAGCCTGTGCGTGGCTGAGTTCGGCGCG 120  
Db 177 TTCTTAGTGGGCTCGGCCAAGCCTGTGCGCCAGCCTGTGCGTGGCTGAGTTCGGCGCG 236  
QY 121 GAGCGCGGGCGGAGCCTGTGCGCAACCCCTCGGACACCTCAACCCGCTGAAGTCTCTG 180  
Db 237 GAGCGCGGGCGGAGCCTGTGCGCAACCCCTCGGACACCTCAACCCGCTGAAGTCTCTG 296  
QY 181 CTGAGCAGCCTGGGATCCCTGTGAACCACTCATAGAGGGTCCCAAGAGTGTGCT 240  
Db 297 CTGAGCAGCCTGGGATCCCTGTGAACCACTCATAGAGGGTCCCAAGAGTGTGCT 356  
QY 241 GAGCTGGGTCCCAAGGCGTGGGGCGTGAAGGCCCTGAAGGCCCTGCTGGGGGCCCTG 300  
Db 357 GAGCTGGGTCCCAAGGCGTGGGGCGTGAAGGCCCTGAAGGCCCTGCTGGGGGCCCTG 416  
QY 301 ACAGTGTGTCG 312  
Db 417 ACAGTGTGTCG 428

RESULT 4  
US-10-211-858-27  
; Sequence 27, Application US/10211858  
; Publication No. US20030211096A1  
; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi J.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Hillan, Kenneth J.  
; APPLICANT: Marsters, Scott A.  
; APPLICANT: Pan, James  
; APPLICANT: Pitti, Robert M.  
; APPLICANT: Roy, Margaret Ann  
; APPLICANT: Smith, Victoria  
; APPLICANT: Stone, Donna M.  
; APPLICANT: Watarabe, Colin K.



APPLICANT: Wood, William I.  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE TREATMENT OF TUMOR  
; FILE REFERENCE: P2931R1C1  
; CURRENT APPLICATION NUMBER: US/10/211,858  
; CURRENT FILING DATE: 2002-08-02  
; PRIOR APPLICATION NUMBER: 60/014699  
; PRIOR FILING DATE: 1996-04-01  
; PRIOR APPLICATION NUMBER: 60/026943  
; PRIOR FILING DATE: 1996-09-23  
; PRIOR APPLICATION NUMBER: 60/059121  
; PRIOR FILING DATE: 1997-07-17  
; PRIOR APPLICATION NUMBER: 60/059352  
; PRIOR FILING DATE: 1997-09-19  
; PRIOR APPLICATION NUMBER: 60/062037  
; PRIOR FILING DATE: 1997-10-10  
; PRIOR APPLICATION NUMBER: 60/063755  
; PRIOR FILING DATE: 1997-10-17  
; PRIOR APPLICATION NUMBER: 60/063045  
; PRIOR FILING DATE: 1997-10-24  
; PRIOR APPLICATION NUMBER: 60/063046  
; PRIOR FILING DATE: 1997-10-24  
; PRIOR APPLICATION NUMBER: 60/066511  
; PRIOR FILING DATE: 1997-11-24  
; PRIOR APPLICATION NUMBER: 60/066772  
; PRIOR FILING DATE: 1997-11-24  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 258  
; SEQ ID NO 27  
; LENGTH: 569  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-211-858-27

Query Match 99.0%; Score 308.8; DB 13; Length 569;  
Best Local Similarity 99.4%; Pred. No. 4.6e-67;  
Matches 310; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 1 ATGAAGCTCGCGCCCTCTGGGCTCTGGCTGGCCCTGTCTGCAGCTCGCTCGTGTCT 60  
Db 79 ATGAAGCTCGCGCCCTCTGGGCTCTGGCTGGCCCTGTCTGCAGCTCGCTCGTGTCT 138  
QY 61 TTCTTAGTGGCTCGGCAAGCCCTGTGGCCAGCTGTGCTGGCTGGCTGGCTGGCTGGCT 120  
Db 139 TTCTTAGTGGCTCGGCAAGCCCTGTGGCCAGCTGTGCTGGCTGGCTGGCTGGCTGGCT 198  
QY 121 GAGCGCGGGCGGAGCCCTGGCCAAACCCCTCGGCACCTCAACCCGCTGAAGCTCTCTG 180  
Db 199 GAGCGCGGGCGGAGCCCTGGCCAAACCCCTCGGCACCTCAACCCGCTGAAGCTCTCTG 258  
QY 181 CTGAGCAGCTGGGCATCCCGCTGAACCACTCATAGAGGCTCCAGAGCTGTGTGGCT 240  
Db 259 CTGAGCAGCTGGGCATCCCGCTGAACCACTCATAGAGGCTCCAGAGCTGTGTGGCT 318  
QY 241 GAGCTGGTCCCGAGGCGCTGGGGCGCTGAAGCCCTGAAGCCCTGTCTGGGGCGCCCTG 300  
Db 319 GAGCTGGTCCCGAGGCGCTGGGGCGCTGAAGCCCTGAAGCCCTGTCTGGGGCGCCCTG 378  
QY 301 ACAGTGTGGC 312  
Db 379 ACAGTGTGGC 390

## RESULT 5

US-10-210-951-27  
; Sequence 27, Application US/10210951  
; Publication No. US20030170228A1  
; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi J.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Hillan, Kenneth J.  
; APPLICANT: Marsters, Scott A.

APPLICANT: Pan, James  
; APPLICANT: Pitti, Robert M.  
; APPLICANT: Roy, Margaret Ann  
; APPLICANT: Smith, Victoria  
; APPLICANT: Stone, Donna M.  
; APPLICANT: Watanabe, Colin K.  
; APPLICANT: Wood, William I.  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE TREATMENT OF TUMOR  
; FILE REFERENCE: P2931R1C1  
; CURRENT APPLICATION NUMBER: US/10/210,951  
; CURRENT FILING DATE: 2002-08-02  
; PRIOR APPLICATION NUMBER: 60/014699  
; PRIOR FILING DATE: 1996-04-01  
; PRIOR APPLICATION NUMBER: 60/026943  
; PRIOR FILING DATE: 1996-09-23  
; PRIOR APPLICATION NUMBER: 60/059121  
; PRIOR FILING DATE: 1997-07-17  
; PRIOR APPLICATION NUMBER: 60/059352  
; PRIOR FILING DATE: 1997-09-19  
; PRIOR APPLICATION NUMBER: 60/062037  
; PRIOR FILING DATE: 1997-10-10  
; PRIOR APPLICATION NUMBER: 60/063755  
; PRIOR FILING DATE: 1997-10-17  
; PRIOR APPLICATION NUMBER: 60/063045  
; PRIOR FILING DATE: 1997-10-24  
; PRIOR APPLICATION NUMBER: 60/063046  
; PRIOR FILING DATE: 1997-10-24  
; PRIOR APPLICATION NUMBER: 60/066511  
; PRIOR FILING DATE: 1997-11-24  
; PRIOR APPLICATION NUMBER: 60/066772  
; PRIOR FILING DATE: 1997-11-24  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 258  
; SEQ ID NO 27  
; LENGTH: 569  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-210-951-27

Query Match 99.0%; Score 308.8; DB 15; Length 569;  
Best Local Similarity 99.4%; Pred. No. 4.6e-67;  
Matches 310; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 1 ATGAAGCTCGCGCCCTCTGGGCTCTGGCTGGCCCTGTCTGCAGCTCGCTCGTGTCT 60  
Db 79 ATGAAGCTCGCGCCCTCTGGGCTCTGGCTGGCCCTGTCTGCAGCTCGCTCGTGTCT 138  
QY 61 TTCTTAGTGGCTCGGCAAGCCCTGTGGCCAGCTGTGCTGGCTGGCTGGCTGGCTGGCT 120  
Db 139 TTCTTAGTGGCTCGGCAAGCCCTGTGGCCAGCTGTGCTGGCTGGCTGGCTGGCTGGCT 198  
QY 121 GAGCGCGGGCGGAGCCCTGGCCAAACCCCTCGGCACCTCAACCCGCTGAAGCTCTCTG 180  
Db 199 GAGCGCGGGCGGAGCCCTGGCCAAACCCCTCGGCACCTCAACCCGCTGAAGCTCTCTG 258  
QY 181 CTGAGCAGCTGGGCATCCCGCTGAACCACTCATAGAGGCTCCAGAGCTGTGTGGCT 240  
Db 259 CTGAGCAGCTGGGCATCCCGCTGAACCACTCATAGAGGCTCCAGAGCTGTGTGGCT 318  
QY 241 GAGCTGGTCCCGAGGCGCTGGGGCGCTGAAGCCCTGAAGCCCTGTCTGGGGCGCCCTG 300  
Db 319 GAGCTGGTCCCGAGGCGCTGGGGCGCTGAAGCCCTGAAGCCCTGTCTGGGGCGCCCTG 378  
QY 301 ACAGTGTGGC 312  
Db 379 ACAGTGTGGC 390

## RESULT 6

US-10-211-884-27  
; Sequence 27, Application US/10211884  
; Publication No. US20030175900A1  
; GENERAL INFORMATION:

APPLICANT: Ashkenazi, Avi J.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Gurney, Austin L.  
APPLICANT: Hillan, Kenneth J.  
APPLICANT: Marsters, Scott A.  
APPLICANT: Pan, James  
APPLICANT: Pitti, Robert M.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Smith, Victoria  
APPLICANT: Stone, Donna M.  
APPLICANT: Watanabe, Colin K.  
APPLICANT: Wood, William I.

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE TREATMENT OF TUMOR

FILE REFERENCE: P2931R1C1

CURRENT APPLICATION NUMBER: US/10/211,884

PRIOR APPLICATION NUMBER: 2002-08-02

PRIOR FILING DATE: 1996-04-01

PRIOR APPLICATION NUMBER: 60/026943

PRIOR FILING DATE: 1996-09-23

PRIOR APPLICATION NUMBER: 60/059121

PRIOR FILING DATE: 1997-07-17

PRIOR APPLICATION NUMBER: 60/059352

PRIOR FILING DATE: 1997-09-19

PRIOR APPLICATION NUMBER: 60/062037

PRIOR FILING DATE: 1997-10-10

PRIOR APPLICATION NUMBER: 60/063755

PRIOR FILING DATE: 1997-10-17

PRIOR APPLICATION NUMBER: 60/063045

PRIOR FILING DATE: 1997-10-24

PRIOR APPLICATION NUMBER: 60/063046

PRIOR FILING DATE: 1997-10-24

PRIOR APPLICATION NUMBER: 60/066511

PRIOR FILING DATE: 1997-11-24

PRIOR APPLICATION NUMBER: 60/066772

PRIOR FILING DATE: 1997-11-24

Remaining Prior Application data removed - See File Wrapper or PALM.

NUMBER OF SEQ ID NOS: 258

SEQ ID NO 27

LENGTH: 569

TYPE: DNA

ORGANISM: Homo sapiens

US-10-211-884-27

Query Match 99.0%; Score 308.8; DB 15; Length 569;  
Best Local Similarity 99.4%; Pred No. 4.6e-67;  
Matches 310; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ATGAAGCTCGCGCCCTCTCGGGGCTCTGCGTGGCCCTGTCTCTGAGCTCGCTCGTGCCT 60  
DB 79 ATGAAGCTCGCGCCCTCTCGGGGCTCTGCGTGGCCCTGTCTCTGAGCTCGCTCGTGCCT 138  
QY 61 TTCTTAGTGGGCTGGCCCAAGCTGTGGCCAGCTGTGCTGCGTGGCTGAGTGGCGCG 120  
DB 139 TTCTTAGTGGGCTGGCCCAAGCTGTGGCCAGCTGTGCTGCGTGGCTGAGTGGCGCG 198  
QY 121 GAGGCGGGGCGGACCTCTGSCCAACCCCTCGGCACCTCAACCCCTGAAGTCTCTG 180  
DB 199 GAGGCGGGGCGGACCTCTGSCCAACCCCTCGGCACCTCAACCCCTGAAGTCTCTG 258  
QY 181 CTGAGCAGCTGGGCATCCCGTGAACCACTCAATAGAGGCTCTCCAGAGTGTGTGCT 240  
DB 259 CTGAGCAGCTGGGCATCCCGTGAACCACTCAATAGAGGCTCTCCAGAGTGTGTGCT 318  
QY 241 GAGCTGGTCCCGAGGCGCTGGGGCCCTGAAGCCCTGAAGCCCTGAGGGCCCTG 300  
DB 319 GAGCTGGTCCCGAGGCGCTGGGGCCCTGAAGCCCTGAAGCCCTGAGGGCCCTG 378  
QY 301 ACAGTGTGTGGC 312  
DB 379 ACAGTGTGTGGC 390

## RESULT 7

US-09-989-722-407

Sequence 407, Application US/09989722

Patent No. US20020072067A1

GENERAL INFORMATION:

APPLICANT: Ashkenazi, Avi J.

APPLICANT: Baker, Kevin P.

APPLICANT: Botstein, David

APPLICANT: Desnovers, Luc

APPLICANT: Eaton, Dan L.

APPLICANT: Ferrara, Napoleone

APPLICANT: Fong, Sherman

APPLICANT: Gerber, Hanspeter

APPLICANT: Gerritsen, Mary E.

APPLICANT: Goddard, Audrey

APPLICANT: Godowski, Paul J.

APPLICANT: Grimaldi, J. Christopher

APPLICANT: Gurney, Austin L.

APPLICANT: Kljavin, Ivar J.

APPLICANT: Napier, Mary A.

APPLICANT: Pan, James

APPLICANT: Paoni, Nicholas F.

APPLICANT: Roy, Margaret Ann

APPLICANT: Stewart, Timothy A.

APPLICANT: Tumas, Daniel

APPLICANT: Watanabe, Colin K.

APPLICANT: Williams, P. Mickey

APPLICANT: Wood, William I.

APPLICANT: Zhang, Zemin

TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

Acids Encoding the Same

FILE REFERENCE: P2730P1C63

CURRENT APPLICATION NUMBER: US/09/989,722

CURRENT FILING DATE: 2001-11-19

PRIOR APPLICATION NUMBER: 60/049787

PRIOR FILING DATE: 1997-06-16

PRIOR APPLICATION NUMBER: 60/062250

PRIOR FILING DATE: 1997-10-17

PRIOR APPLICATION NUMBER: 60/065186

PRIOR FILING DATE: 1997-11-12

PRIOR APPLICATION NUMBER: 60/065311

PRIOR FILING DATE: 1997-11-13

PRIOR APPLICATION NUMBER: 60/066770

PRIOR FILING DATE: 1997-11-24

PRIOR APPLICATION NUMBER: 60/075945

PRIOR FILING DATE: 1998-02-25

PRIOR APPLICATION NUMBER: 60/078910

PRIOR FILING DATE: 1998-03-20

PRIOR APPLICATION NUMBER: 60/083322

PRIOR FILING DATE: 1998-04-28

PRIOR APPLICATION NUMBER: 60/084600

PRIOR FILING DATE: 1998-05-07

PRIOR APPLICATION NUMBER: 60/087106

PRIOR FILING DATE: 1998-05-28

PRIOR APPLICATION NUMBER: 60/087607

PRIOR FILING DATE: 1998-06-02

PRIOR APPLICATION NUMBER: 60/087609

PRIOR FILING DATE: 1998-06-02

PRIOR APPLICATION NUMBER: 60/087759

PRIOR FILING DATE: 1998-06-02

PRIOR APPLICATION NUMBER: 60/087827

PRIOR FILING DATE: 1998-06-03

PRIOR APPLICATION NUMBER: 60/088021

PRIOR FILING DATE: 1998-06-04

PRIOR APPLICATION NUMBER: 60/088025

PRIOR FILING DATE: 1998-06-04

PRIOR APPLICATION NUMBER: 60/088026

PRIOR FILING DATE: 1998-06-04

PRIOR APPLICATION NUMBER: 60/088028

PRIOR FILING DATE: 1998-06-04

PRIOR APPLICATION NUMBER: 60/088029

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;; PRIOR FILING DATE: 1998-06-24  
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;; PRIOR FILING DATE: 1998-06-26  
;; PRIOR APPLICATION NUMBER: 60/091360  
;; PRIOR FILING DATE: 1998-07-01  
;; PRIOR APPLICATION NUMBER: 60/091478  
;; PRIOR FILING DATE: 1998-07-02  
;; PRIOR APPLICATION NUMBER: 60/091544  
;; PRIOR FILING DATE: 1998-07-01  
;; PRIOR APPLICATION NUMBER: 60/091519  
;; PRIOR FILING DATE: 1998-07-02  
;; PRIOR APPLICATION NUMBER: 60/091626  
;; PRIOR FILING DATE: 1998-07-02  
;; PRIOR APPLICATION NUMBER: 60/091633  
;; PRIOR FILING DATE: 1998-07-02  
;; PRIOR APPLICATION NUMBER: 60/091978  
;; PRIOR FILING DATE: 1998-07-07  
;; PRIOR APPLICATION NUMBER: 60/091982  
;; PRIOR FILING DATE: 1998-07-07  
;; PRIOR APPLICATION NUMBER: 60/092182  
;; PRIOR FILING DATE: 1998-07-09

Query Match 99.0%; Score 308.8; DB 9; Length 570;

Best Local Similarity 99.4%; Pred. No. 4.6e-67;

Matches 310; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY	1	ATGAAGCTCGCGCCCTCTCGGGGCTCTGCGGCCCTGTGGCCAGCCTGTGGCCAGCCTGTGGCTGCGCTGAGTCGCGCGG	60
Db	79	ATGAAGCTCGCGCCCTCTCGGGGCTCTGCGGCCCTGTGGGCTGTGGGCTGTGGCTGCGCTGAGTCGCGCGG	138
QY	61	TTCTTAGTGGGCTCGGCCAAGCCTGTGGCCAGCCTGTGGCTGCGCTGAGTCGCGCGG	120
Db	139	TTCTTAGTGGGCTCGGCCAAGCCTGTGGCCAGCCTGTGGCTGCGCTGAGTCGCGCGG	198
QY	121	GAGCGCGGCGCGGACCGCTGCGCAACCCCTGCGCACCTCAACCCGCTGAAGTCCTG	180
Db	199	GAGCGCGGCGCGGACCGCTGCGCAACCCCTGCGCACCTCAACCCGCTGAAGTCCTG	258



Matches	310;	Conservative	0;	Mismatches	2;	Indels	0;	Gaps	0;
QY	1	ATGAAGCTCGCCGCCCTCCTCGGTGGGCGCTCTGGGTGGCCCTGTCTTCAGTCCGCTCGTGCT	60						
Db	79	AUGAAGCTCGCCGCCCTCCTCGGTGGGCGCTCTGGTGGCCCTGTCTTCAGTCCGCTCGTGCT	138						
QY	61	TTCATTAGTGGCTCGGCCAAGACCTGTGGGCCAGCTGTGCTGCGCTGGAGTCCGGCGCG	120						
Db	139	TTCATTAGTGGCTCGGCCAAGACCTGTGGGCCAGCTGTGCTGCGCTGGAGTCCGGCGCG	198						
QY	121	GAGGCGGGCGCGGACCCTGGGCAAACCCCCTCGGCACCTCAACCCGCTGAAGCTCTCGT	180						
Db	199	GAGGCGGGCGCGGACCCTGGGCAAACCCCCTCGGCACCTCAACCCGCTGAAGCTCTCGT	258						
QY	181	CTGAGCAGACTGGGGCATCCCCGTGAACCACTCATAGAGGGCTCCCAAGAAGTGTGTGGCT	240						
Db	259	CTGAGCAGACTGGGGCATCCCCGTGAACCACTCATAGAGGGCTCCCAAGAAGTGTGTGGCT	318						
QY	241	GAGCTGGGTCCCGAGCGCGTGGGGCGCGTGAAGGCCCTGAAAGGCCCTGTCTGGGGGCCCTG	300						
Db	319	GAGCTGGGTCCCGAGCGCGTGGGGCGCGTGAAGGCCCTGAAAGGCCCTGTCTGGGGGCCCTG	378						
QY	301	ACAGTCTTTGGC	312						
Db	379	ACAGTCTTTGGC	390						

RESULT 9  
US-09-989-279-407  
Sequence 407, Application US/09989279  
Patent No. US20020072496A1  
GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi J.  
APPLICANT: Baker, Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dan L.  
APPLICANT: Ferrara, Napoleone  
APPLICANT: Fong, Sherman  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gerritsen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gurney, Austin L.  
APPLICANT: Kljavin, Ivar J.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Watanabe, Colin K.  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic Acids Encoding the Same  
FILE REFERENCE: P2730PIC56  
CURRENT APPLICATION NUMBER: US/09/989, 279  
CURRENT FILING DATE: 2001-11-19  
PRIOR APPLICATION NUMBER: 60/049787  
PRIOR FILING DATE: 1997-06-16  
PRIOR APPLICATION NUMBER: 60/062250  
PRIOR FILING DATE: 1997-10-17  
PRIOR APPLICATION NUMBER: 60/065186  
PRIOR FILING DATE: 1997-11-12  
PRIOR APPLICATION NUMBER: 60/065311  
PRIOR FILING DATE: 1997-11-13  
PRIOR APPLICATION NUMBER: 60/066770  
PRIOR FILING DATE: 1997-11-24  
PRIOR APPLICATION NUMBER: 60/075945  
PRIOR FILING DATE: 1998-02-25

PRIOR FILING DATE: 1997-11-24  
PRIOR APPLICATION NUMBER: 60/075945  
PRIOR FILING DATE: 1998-02-25

[illegible]

;; PRIOR APPLICATION NUMBER: 60/091626  
;; PRIOR FILING DATE: 1998-07-02  
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;; PRIOR APPLICATION NUMBER: 60/091978  
;; PRIOR FILING DATE: 1998-07-07  
;; PRIOR APPLICATION NUMBER: 60/091982  
;; PRIOR FILING DATE: 1998-07-07  
;; PRIOR APPLICATION NUMBER: 60/092182  
;; PRIOR FILING DATE: 1998-07-09

Query Match 99.0%; Score 308.8; DB 9; Length 570;

Best Local Similarity 99.4%; Pred. No. 4.6e-67;

Matches 310; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ATCAAGCTCCCGCCCTCTCGGGGCTCTGGTGGCCCTGCTGAGCTCGCTCGGTGCT 60  
DB 79 ATGAAGCTCCCGCCCTCTCGGGGCTCTGGTGGCCCTGCTGAGCTCGGTGCT 138  
QY 61 TTCTTAGTGGGCTCGGCCAAGCCTGTGGCCAGCCTGTCTGCTGGCTGGAGTCGGGGCG 120  
DB 139 TTCTTAGTGGGCTCGGCCAAGCCTGTGGCCAGCCTGTCTGCTGGCTGGAGTCGGGGCG 198  
QY 121 GAGCCCGGGCCGGGACCTTGGCCAAACCCCTCGGACCCCTCAACCCGCTGAAGCTCCTG 180  
DB 199 GAGCCCGGGCCGGGACCTTGGCCAAACCCCTCGGACCCCTCAACCCGCTGAAGCTCCTG 258  
QY 181 CTGAGCAGCCTGGGCATCCCGCTGAACCACTCATAGAGGCTCCCAAGAGTGTGGCT 240  
DB 259 CTGAGCAGCCTGGGCATCCCGCTGAACCACTCATAGAGGCTCCCAAGAGTGTGGCT 318  
QY 241 GAGCTGGTCCCGCAGGCGGTGGGGCGGTGAAGGCCCTGGAAGGCCCTGCTGGGGGCCCTG 300  
DB 319 GAGCTGGTCCCGCAGGCGGTGGGGCGGTGAAGGCCCTGGAAGGCCCTGCTGGGGGCCCTG 378  
QY 301 ACAGTGTGGC 312  
DB 379 ACAGTGTGGC 390

## RESULT 10

US-09-989-727-407

Sequence 407, Application US/09989727

Patent No. US20020072497A1

GENERAL INFORMATION:

APPLICANT: Ashkenazi, Avi J.

APPLICANT: Baker, Kevin P.

APPLICANT: Botstein, David

APPLICANT: Desnoyers, Luc

APPLICANT: Eaton, Dan L.

APPLICANT: Ferrara, Napoleone

APPLICANT: Fong, Sherman

APPLICANT: Gerber, Hanspeter

APPLICANT: Gerritsen, Mary E.

APPLICANT: Goddard, Audrey

APPLICANT: Godowski, Paul J.

APPLICANT: Grimaldi, J. Christopher

APPLICANT: Gurney, Austin L.

APPLICANT: Kljavin, Ivar J.

APPLICANT: Napier, Mary A.

APPLICANT: Pan, James

APPLICANT: Paoni, Nicholas F.

APPLICANT: Roy, Margaret Ann

APPLICANT: Stewart, Timothy A.

APPLICANT: Tumas, Daniel

APPLICANT: Watanabe, Colin K.

APPLICANT: Williams, P. Mickey

APPLICANT: Wood, William I.

APPLICANT: Zhang, Zemin

TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
Acids Encoding the Same

FILE REFERENCE: P2730P1C65

CURRENT APPLICATION NUMBER: US/09/989,727

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;; PRIOR APPLICATION NUMBER: 60/049787  
;; PRIOR FILING DATE: 1997-06-16  
;; PRIOR APPLICATION NUMBER: 60/062250  
;; PRIOR FILING DATE: 1997-10-17  
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; PRIOR FILING DATE: 1998-07-02  
; PRIOR APPLICATION NUMBER: 60/091978  
; PRIOR FILING DATE: 1998-07-07  
; PRIOR APPLICATION NUMBER: 60/091982  
; PRIOR FILING DATE: 1998-07-07  
; PRIOR APPLICATION NUMBER: 60/092182  
; PRIOR FILING DATE: 1998-07-09  
  
Query Match 99.0%; Score 308.8; DB 9; Length 570;  
Best Local Similarity 99.4%; Pred. No. 4.6e-67;  
Matches 310; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
  
QY 1 ATGAAGCTGGCGCCCTCTGCGGGGCTCTGCGTGGCCCTCTGCGAGCTCCGCTCGTCTGCT 60  
Db 79 ATGAAGCTGGCGCCCTCTGCGGGGCTCTGCGTGGCCCTCTGCGAGCTCCGCTCGTCTGCT 138  
  
QY 61 TTCTTAGTGGCTCGCGCCCAAGCCTGTGCGCCAGCCTGTGCGTGGCTGGAGTGGCGGCG 120  
Db 139 TTCTTAGTGGCTCGCGCCCAAGCCTGTGCGCCAGCCTGTGCGTGGCTGGAGTGGCGGCG 198  
  
QY 121 GAGCGCGGGCGCGGACCCCTGGCCAAACCCCTCGGACCCCTCAACCCGCTGAAGCTCTCTG 180  
Db 199 GAGCGCGGGCGCGGACCCCTGGCCAAACCCCTCGGACCCCTCAACCCGCTGAAGCTCTCTG 258  
  
QY 181 CTGAGCAGCTGGGCGATCCCGTGAACCACTCTATAGGGGCTCCAGAGTGTGTGCT 240  
Db 259 CTGAGCAGCTGGGCGATCCCGTGAACCACTCTATAGGGGCTCCAGAGTGTGTGCT 318  
  
QY 241 GAGCTGGTCCCGCAGGCGGTGGGGCGCGTGAAGGCCCTGCTGGGGGCCCTG 300  
Db 319 GAGCTGGTCCCGCAGGCGGTGGGGCGCGTGAAGGCCCTGCTGGGGGCCCTG 378  
  
QY 301 ACAGTGTGTTGGC 312  
Db 379 ACAGTGTGTTGGC 390  
  
RESULT 11  
US-09-989-731-407  
; Sequence 407, Application US/09989731  
; Patent No. US20020103125A1  
; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi J.  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan L.  
; APPLICANT: Ferrara, Napoleone  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gerber, Hanspeter  
; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Kljavin, Ivar J.  
; APPLICANT: Napier, Mary A.



APPLICANT: Pan,James  
APPLICANT: Paoni,Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Watanabe, Colin K.  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
TITLE OF INVENTION: Acids Encoding the Same  
FILE REFERENCE: P2730PIC70  
CURRENT APPLICATION NUMBER: US/09/989,731  
CURRENT FILING DATE: 2001-11-20  
PRIOR APPLICATION NUMBER: 60/049787  
PRIOR FILING DATE: 1997-06-16  
PRIOR APPLICATION NUMBER: 60/062250  
PRIOR FILING DATE: 1997-10-17  
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PRIOR APPLICATION NUMBER: 60/066770  
PRIOR FILING DATE: 1997-11-24  
PRIOR APPLICATION NUMBER: 60/075945  
PRIOR FILING DATE: 1998-02-25  
PRIOR APPLICATION NUMBER: 60/078910  
PRIOR FILING DATE: 1998-03-20  
PRIOR APPLICATION NUMBER: 60/083322  
PRIOR FILING DATE: 1998-04-28  
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;; PRIOR FILING DATE: 1998-07-09

Query Match 99.0%; Score 308.8; DB 9; Length 570;

Best Local Similarity 99.4%; Pred. No. 4.6e-67;

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Qy 181 CTGACAGCCTGGGATCCCGTGACCACTCATAGAGGCTCCAGAGTGTGCTGCT 240  
Db 259 CTGACAGCCTGGGATCCCGTGACCACTCATAGAGGCTCCAGAGTGTGCTGCTGCT 318  
Qy 241 GAGCTGGTCCCGAGCGTGGGCGCGGTGAGGCGCTGAGGCGCTGAGGCGCGCTG 300  
Db 319 GAGCTGGTCCCGAGCGTGGGCGCGGTGAGGCGCTGAGGCGCTGAGGCGCGCTG 378  
Qy 301 ACAGTGTGCTGGC 312  
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RESULT 12

US-09-989-732-407

; Sequence 407, Application US/09989732

; Patent No. US20020123463A1

; GENERAL INFORMATION:

; APPLICANT: Ashkenazi, Avi J.

; APPLICANT: Baker, Kevin P.

;; APPLICANT: Botstein, David  
;; APPLICANT: Desnoyers, Luc  
;; APPLICANT: Eaton, Dan L.  
;; APPLICANT: Ferrara, Napoleone  
;; APPLICANT: Fong, Sherman  
;; APPLICANT: Gerber, Hanspeter  
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;; APPLICANT: Goddard, Audrey  
;; APPLICANT: Godowski, Paul J.  
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;; APPLICANT: Napier, Mary A.  
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;; APPLICANT: Stewart, Timothy A.  
;; APPLICANT: Tumas, Daniel  
;; APPLICANT: Watanabe, Colin K.  
;; APPLICANT: Williams, P. Mickey  
;; APPLICANT: Wood, William I.  
;; APPLICANT: Zhang, Zemin  
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;; TITLE OF INVENTION: Acids Encoding the Same  
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/	PRIOR FILING DATE:	1998-07-09
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Best Local Similarity    99.4%; Pred. No. 4.6e-67;		
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Db	139	TTCATTAGTGGGCTCGGCCAAGCCTGTGGCCCCAGCCTGTGCTGCCTGTGAGTTCGGCGCGCG 198
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Sequence 407, Application US/09991073  
Patent No. US2002012756A1  
GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi J.  
APPLICANT: Baker, Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Desnovers, Luc  
APPLICANT: Eaton, Dan L.  
APPLICANT: Ferrara, Napoleone  
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APPLICANT: Watanabe, Colin K.  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
APPLICANT: Zhang, Zemin

TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
Acids Encoding the Same  
FILE REFERENCE: P2730P1C15  
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;; PRIOR FILING DATE: 1998-06-25  
;; PRIOR APPLICATION NUMBER: 60/090862  
;; PRIOR FILING DATE: 1998-06-26  
;; PRIOR APPLICATION NUMBER: 60/090863  
;; PRIOR FILING DATE: 1998-06-26  
;; PRIOR APPLICATION NUMBER: 60/091360  
;; PRIOR FILING DATE: 1998-07-01  
;; PRIOR APPLICATION NUMBER: 60/091478

;; PRIOR FILING DATE: 1998-07-02  
;; PRIOR APPLICATION NUMBER: 60/091544  
;; PRIOR FILING DATE: 1998-07-01  
;; PRIOR APPLICATION NUMBER: 60/091519  
;; PRIOR FILING DATE: 1998-07-02  
;; PRIOR APPLICATION NUMBER: 60/091626  
;; PRIOR FILING DATE: 1998-07-02  
;; PRIOR APPLICATION NUMBER: 60/091633  
;; PRIOR FILING DATE: 1998-07-02  
;; PRIOR APPLICATION NUMBER: 60/091978  
;; PRIOR FILING DATE: 1998-07-07  
;; PRIOR APPLICATION NUMBER: 60/091982  
;; PRIOR FILING DATE: 1998-07-07  
;; PRIOR APPLICATION NUMBER: 60/092182  
;; PRIOR FILING DATE: 1998-07-09

Query Match 99.0%; Score 308.8; DB 9; Length 570;  
Best Local Similarity 99.4%; Pred. No. 4.6e-67;  
Matches 310; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 ATGAAGCTCGCCCGCTCTCTGCGGCTCTGCGTGGCCCTGTCTGCGAGCTCCGCTCGTGTCT 60  
|||  
Db 79 ATGAAGCTCGCCCGCTCTCTGCGGCTCTGCGTGGCCCTGTCTGCGAGCTCCGCTCGTGTCT 138  
|||

Qy 61 TTCTTAGTGGGCTCGGCCAAGCCTGTGGCCCAAGCCTGTGGCCCAAGCCTGTGGCCCAAGCCTGTGG 120  
|||

Db 139 TTCTTAGTGGGCTCGGCCAAGCCTGTGGCCCAAGCCTGTGGCCCAAGCCTGTGGCCCAAGCCTGTGG 198  
|||

Qy 121 GAGGCCGGGGCGGGACCTGCGCCAAACCCCTGGCCAAACCCCTGGCCAAACCCCTGGCCAAACCCCTGG 180  
|||

Db 199 GAGGCCGGGGCGGGACCTGCGCCAAACCCCTGGCCAAACCCCTGGCCAAACCCCTGGCCAAACCCCTGG 258  
|||

Qy 181 CTGAGCAGCCTGCGGCATCCCGGTGAACCCACCTCATAGAGGGCTCCCGAGAGTGTGTGGCT 240  
|||

Db 259 CTGAGCAGCCTGCGGCATCCCGGTGAACCCACCTCATAGAGGGCTCCCGAGAGTGTGTGGCT 318  
|||

Qy 241 GAGCTGGTCCCAGAGCCCGTGGGGCCCGTGAAGGCCCTGAAGGCCCTGAAGGCCCTGAAGGCCCTGAAG 300  
|||

Db 319 GAGCTGGTCCCAGAGCCCGTGGGGCCCGTGAAGGCCCTGAAGGCCCTGAAGGCCCTGAAGGCCCTGAAG 378  
|||

Qy 301 ACAGTGTTTGGC 312  
|||

Db 379 ACAGTGTTTGGC 390  
|||

Search completed: June 6, 2004, 16:47:38  
Job time : 328 secs



GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: June 6, 2004, 17:58:17 ; Search time 417 Seconds  
(without alignments)  
6159.242 Million cell updates/sec

Title: SEQ19PLUS12

Perfect score: 563

Sequence: 1 cgcgcggaggcgccggg.....ccgcgcggcgccggggagg 563

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 2995936 seqs, 2280998010 residues

Total number of hits satisfying chosen parameters: 5991872

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications NA: \*

- 1: /cgn2\_6/ptodata/2/pubpna/US07\_PUBCOMB.seq:\*
- 2: /cgn2\_6/ptodata/2/pubpna/PCT\_NEW\_PUB.seq:\*
- 3: /cgn2\_6/ptodata/2/pubpna/US06\_NEW\_PUB.seq:\*
- 4: /cgn2\_6/ptodata/2/pubpna/US06\_PUBCOMB.seq:\*
- 5: /cgn2\_6/ptodata/2/pubpna/US07\_NEW\_PUB.seq:\*
- 6: /cgn2\_6/ptodata/2/pubpna/PCTUS\_PUBCOMB.seq:\*
- 7: /cgn2\_6/ptodata/2/pubpna/US08\_NEW\_PUB.seq:\*
- 8: /cgn2\_6/ptodata/2/pubpna/US08\_PUBCOMB.seq:\*
- 9: /cgn2\_6/ptodata/2/pubpna/US09A\_PUBCOMB.seq:\*
- 10: /cgn2\_6/ptodata/2/pubpna/US09B\_PUBCOMB.seq:\*
- 11: /cgn2\_6/ptodata/2/pubpna/US09C\_PUBCOMB.seq:\*
- 12: /cgn2\_6/ptodata/2/pubpna/US09\_NEW\_PUB.seq:\*
- 13: /cgn2\_6/ptodata/2/pubpna/US09A\_PUBCOMB.seq:\*
- 14: /cgn2\_6/ptodata/2/pubpna/US10A\_PUBCOMB.seq:\*
- 15: /cgn2\_6/ptodata/2/pubpna/US10B\_PUBCOMB.seq:\*
- 16: /cgn2\_6/ptodata/2/pubpna/US10C\_PUBCOMB.seq:\*
- 17: /cgn2\_6/ptodata/2/pubpna/US10\_NEW\_PUB.seq:\*
- 18: /cgn2\_6/ptodata/2/pubpna/US60\_NEW\_PUB.seq:\*
- 19: /cgn2\_6/ptodata/2/pubpna/US60\_PUBCOMB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	509.2	90.4	547	14	US-10-081-817-19
2	338.4	60.1	1794	15	US-10-059-579-120
C 3	143.6	25.5	533	13	US-10-027-632-196114
C 4	143.6	25.5	533	16	US-10-027-632-196114
5	116	20.6	561	15	US-10-237-435-6
6	87	15.5	527	17	US-10-426-002-18
7	78	13.9	569	13	US-10-211-858-27
8	78	13.9	569	15	US-10-210-951-27
9	78	13.9	569	15	US-10-211-884-27
10	78	13.9	570	9	US-09-989-722-407
11	78	13.9	570	9	US-09-989-723-407
12	78	13.9	570	9	US-09-989-279-407
13	78	13.9	570	9	US-09-989-727-407
14	78	13.9	570	9	US-09-989-731-407

15	78	13.9	570	9	US-09-989-732-407	Sequence 407, App
16	78	13.9	570	9	US-09-991-073-407	Sequence 407, App
17	78	13.9	570	9	US-09-990-442-407	Sequence 407, App
18	78	13.9	570	9	US-09-991-163-407	Sequence 407, App
19	78	13.9	570	9	US-09-993-604-407	Sequence 407, App
20	78	13.9	570	9	US-09-990-456-407	Sequence 407, App
21	78	13.9	570	9	US-09-989-721-407	Sequence 407, App
22	78	13.9	570	9	US-09-992-598-407	Sequence 407, App
23	78	13.9	570	9	US-09-989-293A-407	Sequence 407, App
24	78	13.9	570	9	US-09-989-735-407	Sequence 407, App
25	78	13.9	570	9	US-09-990-444-407	Sequence 407, App
26	78	13.9	570	9	US-09-991-181-407	Sequence 407, App
27	78	13.9	570	9	US-09-989-730-407	Sequence 407, App
28	78	13.9	570	9	US-09-990-436-407	Sequence 407, App
29	78	13.9	570	9	US-09-993-687-407	Sequence 407, App
30	78	13.9	570	10	US-09-989-734-407	Sequence 407, App
31	78	13.9	570	10	US-09-997-653-407	Sequence 407, App
32	78	13.9	570	10	US-09-993-667-407	Sequence 407, App
33	78	13.9	570	10	US-09-997-428-407	Sequence 407, App
34	78	13.9	570	10	US-09-997-666-407	Sequence 407, App
35	78	13.9	570	10	US-09-990-438-407	Sequence 407, App
36	78	13.9	570	10	US-09-990-562-407	Sequence 407, App
37	78	13.9	570	10	US-09-990-711-407	Sequence 407, App
38	78	13.9	570	10	US-09-989-726-407	Sequence 407, App
39	78	13.9	570	10	US-09-998-156-407	Sequence 407, App
40	78	13.9	570	10	US-09-990-437-407	Sequence 407, App
41	78	13.9	570	10	US-09-991-157-407	Sequence 407, App
42	78	13.9	570	10	US-09-997-514-407	Sequence 407, App
43	78	13.9	570	10	US-09-997-573-407	Sequence 407, App
44	78	13.9	570	10	US-09-991-172-407	Sequence 407, App
45	78	13.9	570	10	US-09-990-726-407	Sequence 407, App

#### ALIGNMENTS

#### RESULT 1

US-10-081-817-19  
; Sequence 19, Application US/10081817  
; Publication No. US20020183501A1  
; GENERAL INFORMATION:  
; APPLICANT: Polyak, Kornelia  
; APPLICANT: Porter, Dale  
; APPLICANT: Sgroi, Dennis  
; APPLICANT: Krop, Ian  
; TITLE OF INVENTION: HIN-1, A TUMOR SUPPRESSOR GENE  
; FILE REFERENCE: 00530-094001  
; CURRENT APPLICATION NUMBER: US/10/081,817  
; CURRENT FILING DATE: 2002-05-31  
; PRIOR APPLICATION NUMBER: 60/270,973  
; PRIOR FILING DATE: 2001-02-23  
; PRIOR APPLICATION NUMBER: 60/351,908  
; PRIOR FILING DATE: 2002-01-25  
; NUMBER OF SEQ ID NOS: 32  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 19  
; LENGTH: 547  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: 186  
; OTHER INFORMATION: n = C or G  
US-10-081-817-19

Query Match 90.4%; Score 509.2; DB 14; Length 547;

Best Local Similarity 97.8%; Pred. No. 1.5e-109;

Matches 539; Conservative 8; Mismatches 0;

Indels 4; Gaps 2;

QY 1 CGCGCGGGAGCGCGCGGAGTGGAGGCTGTATGTCCTGGCGCTCCACTCCCCAGG 60

Db 1 CGCGCGGGAGCGCGCGGAGTGGAGGCTGTATGTCCTGGCGCTCCACTCCCCAGG 60

QY 61 CGCAGAGGCGCCACAGAGGACCCCGAGCGTGTCCACGGTCTGGGATCAGAGG 120  
Db 61 CGCAGAGGCGCCACAGAGGACCCCGAGCGTGTCCACGGTCTGGGATCAGAGG 120  
QY 121 CAGGACACAGGAGCGAGGAACTGGCGCGCCCGCCCTGCTGCTGGCGCAGGAGCT 180  
Db 121 CAGGACACAGGAGCGAGGAACTGGCGCGCCCGCCCTGCTGCTGGCGCGG---AGGAAGCT 177  
QY 181 CCTCACNAGAGGAAGCTCCCTCACCCGCGCCAGCCCTCGAGGGGGCGCTGGGGTC 240  
Db 178 CCTCACNAGAGGAAGCTCCCTCACCCGCGCCAGCCCTG-AGGGGGCGCTGGGGTC 236  
QY 241 AGACCGCAAGCAGAGGTGCGGGCGGGGCTCTCGCGAGACAAAGCGCGGCGCTGC 300  
Db 237 AGACCGCAAGCAGAGGTGCGGGCGGGGCTCTCGCGAGACAAAGCGCGGCGCTGC 296  
QY 301 CTCTCTCAGAGGGCGCCAGCGCTCTCCAGAGGAAGTCTCGAGGCGCGCGCAGGAGG 360  
Db 297 CTCTCTCAGAGGGCGCCAGCGCTCTCCAGAGGAAGTCTCGAGGCGCGCGCAGGAGG 356  
QY 361 GGGCACGGGCTTCCAGAGGCGCGCGCGCAGCAGGAAGTTGGCCAGGGCACGGCGGTG 420  
Db 357 GGGCACGGGCTTCCAGAGGCGCGCGCGCAGCAGGAAGTTGGCCAGGGCACGGCGGTG 416  
QY 421 AGCGGAGCGGCGAGGGCTTCTCAGAGAGCGCGCGCAGAGCGCGCTGGAGGGCGAGGA 480  
Db 417 AGCGGAGCGGCGAGGGCTTCTCAGAGAGCGCGCGCAGAGCGCGCTGGAGGGCGAGGA 476  
QY 481 CCGGGTATAGAAAGCCCTGCGCGCTTCCCGGGCAGCGAGGTCCCGCGCGCGCCCGA 540  
Db 477 CCGGGTATAGAAAGCCCTGCGCGCTTCCCGGGCAGCGAGGTCCCGCGCGCGCCCGA 536  
QY 541 GCCCGCGCGCC 551  
Db 537 GCCCGCGCGCC 547

## RESULT 2

US-10-059-579-120  
; Sequence 120, Application US/10059579  
; Publication No. US20030138783A1  
; GENERAL INFORMATION:  
; APPLICANT: THE JOHNS HOPKINS UNIVERSITY SCHOOL OF MEDICINE  
; APPLICANT: SUKUMAR, Saraswati  
; APPLICANT: EVRON, Ella  
; APPLICANT: DOOLEY, William C.  
; APPLICANT: DAVIDSON, Nancy  
; APPLICANT: FACKLER, Mary Jo.  
; TITLE OF INVENTION: ABERRANTLY METHYLATED GENES AS MARKERS OF BREAST MALIGNANCY  
; FILE REFERENCE: JHU1630-1  
; CURRENT APPLICATION NUMBER: US/10/059,579  
; PRIOR FILING DATE: 2003-02-03  
; PRIOR APPLICATION NUMBER: US 09/771,357  
; PRIOR FILING DATE: 2001-01-26  
; NUMBER OF SEQ ID NOS: 136  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 120  
; LENGTH: 1794  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc.feature  
; LOCATION: (359)..(359)  
; OTHER INFORMATION: n is any nucleotide  
US-10-059-579-120

Query Match 60.1%; Score 338.4; DB 15; Length 1794;  
Best Local Similarity 97.8%; Pred. No. 5.7e-70;  
Matches 354; Conservative 0; Mismatches 6; Indels 2; Gaps 1;  
QY 190 GAGGAGAGCTCCCTCACCAGCCAGCCCTCGAGGGGGCGCTGGGGTCAGACCCCAA 249  
Db 812 GAGGAGAGCTCCCTCACCAGCCAGCCCTCAGGGGGCGC--TGGGGTCAGACCCCAA 869

QY 250 AGCGAAGGTGCGGCGCGGGTGGGCTTCGGGAGACAAAGCGCGGGGCTTCCTCTCTCAG 309  
Db 870 AGCGAAGGTGCGGCGCGGGTGGGCTTCGGGAGACAAAGCGCGGGGCTTCCTCTCTCAG 929  
QY 310 AGGCGCCAGCGCTGCTCAAGAGAAAGTCTCTAGAGCCCGGGCAGGAGAAAGGGGACGCGG 369  
Db 930 AGGCGCCAGCGCTGCTCAAGAGAAAGTCTCTAGAGCCCGGGCAGGAGAAAGGGGACGCGG 989  
QY 370 CTCTCCAGAGGCGCGCGCGCGAGGAGTGGCCAGGCGACGCGCTGAGCGGAGCG 429  
Db 990 CTCTCCAGGCGCGCGCGCGCGAGGAGTGGCCAGGCGACGCGCTGAGCGGAGCG 1049  
QY 430 GGCAGGCGCTTCTCAGAGGCGCGGGGAGCGCGCTGGAGGGGCGAGACCGGGGTATA 489  
Db 1050 GGCAGGCGCTTCTCAGAGGCGCGGGGAGCGCGCTGGAGGGGCGAGACCGGGGTATA 1109  
QY 490 AGAAGCTCTGCGCTTGGCCCGGGCAGCGCAGGTTCCTCGCGCGCGCGCGCGCGCG 549  
Db 1110 AGAAGCTCTGCGCTTGGCCCGGGCAGCGCAGGTTCCTCGCGCGCGCGCGCGCGCG 1169  
QY 550 CC 551  
Db 1170 CC 1171

## RESULT 3

US-10-027-632-196114/c  
; Sequence 196114, Application US/10027632  
; Publication No. US20020198371A1  
; GENERAL INFORMATION:  
; APPLICANT: Wang, David G.  
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide  
; TITLE OF INVENTION: Polymorphisms in the Human Genome  
; FILE REFERENCE: 108827.129  
; CURRENT APPLICATION NUMBER: US/10/027,632  
; CURRENT FILING DATE: 2002-04-30  
; PRIOR APPLICATION NUMBER: US 60/218,006  
; PRIOR FILING DATE: 2000-07-12  
; PRIOR APPLICATION NUMBER: US 60/198,676  
; PRIOR FILING DATE: 2000-04-20  
; PRIOR APPLICATION NUMBER: US 60/193,483  
; PRIOR FILING DATE: 2000-03-29  
; PRIOR APPLICATION NUMBER: US 60/185,218  
; PRIOR FILING DATE: 2000-02-24  
; PRIOR APPLICATION NUMBER: US 60/167,363  
; PRIOR FILING DATE: 1999-11-23  
; PRIOR APPLICATION NUMBER: US 60/156,358  
; PRIOR FILING DATE: 1999-09-28  
; PRIOR APPLICATION NUMBER: US 60/146,002  
; PRIOR FILING DATE: 1999-08-09  
; NUMBER OF SEQ ID NOS: 325720  
; SOFTWARE: PastSeq for Windows Version 4.0  
; SEQ ID NO 196114  
; LENGTH: 533  
; TYPE: DNA  
; ORGANISM: Human  
US-10-027-632-196114

Query Match 25.5%; Score 143.6; DB 13; Length 533;  
Best Local Similarity 94.8%; Pred. No. 1.4e-24;  
Matches 181; Conservative 0; Mismatches 5; Indels 5; Gaps 3;  
QY 1 CGGCGCGGGAGGCGCGGGAGTGAGCGCTGTGCTCCCTGGCGCTTCCACTTCCCCAGG 60  
Db 189 CGGCGCGGGAGGCGCGGGAGTGAGCGCTGTGCTCCCTGGCGCTTCCACTTCCCCAGG 130  
QY 61 CGCAGAGGCGCCACAGAGACCCCGAGTGCACAGTGCACAGGTCTGGGATCAGAGG 120  
Db 129 CGCAGAGGCGCCACAGAGACCCCGAGTGCACAGTGCACAGGTCTGGGATCAGAGG 70  
QY 121 CA-GGACACAGGAGCAGGAACCTGCGCGCCCGCCCTGCTGCGCGGAGGAGC 179

Db 69 CACGGACAGGAGCCAGGAACTGGCCGCCCC---CGCCCTCCCTGGCGCGA-GGAAGC 14  
 QY 180 TCCCTCACNG 190  
 Db 13 TCCCTCACGG 3

## RESULT 4

US-10-027-632-196114/c  
 ; Sequence 196114, Application US/10027632  
 ; Publication No. US20030204075A9  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Wang, David G.  
 ; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide  
 ; Polymorphisms in the Human Genome  
 ; FILE REFERENCE: 108927.129  
 ; CURRENT APPLICATION NUMBER: US/10/027,632  
 ; PRIOR FILING DATE: 2002-04-30  
 ; PRIOR APPLICATION NUMBER: US 60/218,006  
 ; PRIOR FILING DATE: 2000-07-12  
 ; PRIOR APPLICATION NUMBER: US 60/198,676  
 ; PRIOR FILING DATE: 2000-04-20  
 ; PRIOR APPLICATION NUMBER: US 60/193,483  
 ; PRIOR FILING DATE: 2000-03-29  
 ; PRIOR APPLICATION NUMBER: US 60/185,218  
 ; PRIOR FILING DATE: 2000-02-24  
 ; PRIOR APPLICATION NUMBER: US 60/167,363  
 ; PRIOR FILING DATE: 1999-11-23  
 ; PRIOR APPLICATION NUMBER: US 60/156,358  
 ; PRIOR FILING DATE: 1999-09-28  
 ; PRIOR APPLICATION NUMBER: US 60/146,002  
 ; PRIOR FILING DATE: 1999-08-09  
 ; NUMBER OF SEQ ID NOS: 325720  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 196114  
 ; LENGTH: 533  
 ; TYPE: DNA  
 ; ORGANISM: Human  
 ; US-10-027-632-196114

Query Match 25.5%; Score 143.6; DB 16; Length 533;  
 Best Local Similarity 94.8%; Pred. No. 1.4e-24;  
 Matches 181; Conservative 0; Mismatches 5; Indels 5; Gaps 3;  
 QY 1 CGGCGGGAGCGCGGAGTGAAGGCTGATCGTCCCTGGCGCTCCACCTCCCGCAGG 60  
 Db 189 CGGCGGGAGCGCGGAGTGAAGGCTGATCGTCCCTGGCGCTCCACCTCCCGCAGG 130  
 QY 61 CGCAGAAGCGCCACGAGGACCCCGAGTCCCGAGCTTGGCCACGCTCTGGGATCAGAGG 120  
 Db 129 CGCAGAAGCGCCACGAGGACCCCGAGTCCCGAGCTTGGCCACGCTCTGGGATCAGAGG 70  
 QY 121 CA-GGGACAGGAGCCAGGAACTGCGCGCCCGCCCTGCTCCCTGGCGGAGGAGC 179  
 Db 69 CACGGACAGGAGCCAGGAACTGCGCGCCCGCCCTGCTCCCTGGCGGAGGAGC 14  
 QY 180 TCCCTCACNG 190  
 Db 13 TCCCTCACGG 3

## RESULT 5

US-10-237-435-6  
 ; Sequence 6, Application US/10237435  
 ; Publication No. US20030124580A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Walker, Michael G.  
 ; APPLICANT: Spiro, Peter A.  
 ; APPLICANT: Murry, Lynn E.  
 ; TITLE OF INVENTION: LUNG SURFACTANT MOLECULES  
 ; FILE REFERENCE: PB-0019 US  
 ; CURRENT APPLICATION NUMBER: US/10/237,435  
 ; CURRENT FILING DATE: 2002-09-06

; PRIOR APPLICATION NUMBER: 60/317,822  
 ; PRIOR FILING DATE: 09-07-2001  
 ; NUMBER OF SEQ ID NOS: 9  
 ; SOFTWARE: PERL Program  
 ; SEQ ID NO 6  
 ; LENGTH: 561  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 ; FEATURE:  
 ; NAME/KEY: misc feature  
 ; OTHER INFORMATION: Incyte ID No. US20030124580A1 242745.1  
 ; US-10-237-435-6

Query Match 20.6%; Score 116; DB 15; Length 561;  
 Best Local Similarity 100.0%; Pred. No. 3.7e-18;  
 Matches 116; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 436 GCTTTCTCAGGAGCGGGCGGCGGCGGCGGCTGTGGAGGGCGGAGACCGGGTATAAGAGC 495  
 Db 1 GCTTTCTCAGGAGCGGGCGGCGGCGGCGGCTGTGGAGGGCGGAGGACCGGGTATAAGAGC 60  
 QY 496 CTCGTGGCCTTGGCGGCGGCGGCGGCGGCGGCTTCCCGCGGCGGCGGCGGCGGCGG 551  
 Db 61 CTCGTGGCCTTGGCGGCGGCGGCGGCGGCGGCTTCCCGCGGCGGCGGCGGCGGCGG 116

## RESULT 6

US-10-426-002-18  
 ; Sequence 18, Application US/10426002  
 ; Publication No. US20040101876A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Mintz, Liat  
 ; APPLICANT: Xie, Hanging  
 ; APPLICANT: Dahari, Dvir  
 ; APPLICANT: Levanon, Erez  
 ; APPLICANT: Freilich, Shiri  
 ; APPLICANT: Beck, Nili  
 ; APPLICANT: Zhu, Wei-Yong  
 ; APPLICANT: Wasserman, Alon  
 ; APPLICANT: Hermesh, Chen  
 ; APPLICANT: Azar, Idit  
 ; APPLICANT: Bernstein, Jeanne  
 ; APPLICANT: Rotem Sorek  
 ; TITLE OF INVENTION: METHODS AND SYSTEMS USEFUL FOR ANNOTATING BIOMOLECULAR SEQUENCES  
 ; FILE REFERENCE: 26083  
 ; CURRENT APPLICATION NUMBER: US/10/426,002  
 ; CURRENT FILING DATE: 2003-04-30  
 ; NUMBER OF SEQ ID NOS: 41  
 ; SOFTWARE: PatentIn version 3.1  
 ; SEQ ID NO 18  
 ; LENGTH: 527  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 ; US-10-426-002-18

Query Match 15.5%; Score 87; DB 17; Length 527;  
 Best Local Similarity 100.0%; Pred. No. 2.1e-11;  
 Matches 87; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 465 GCTGAGGGCGGAGACCGGGTATAAGAGCCTCGTGCTTGCCTGGCGGAGCGCGAGGT 524  
 Db 1 GCTGAGGGCGGAGACCGGGTATAAGAGCCTCGTGCTTGCCTGGCGGAGCGCGAGGT 60  
 QY 525 TCCCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 551  
 Db 61 TCCCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 87

## RESULT 7

US-10-211-958-27  
 ; Sequence 27, Application US/10211859  
 ; Publication No. US20030211096A1  
 ; GENERAL INFORMATION:

APPLICANT: Ashkenazi, Avi J.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Gurney, Austin L.  
APPLICANT: Hillan, Kenneth J.  
APPLICANT: Marsters, Scot A.  
APPLICANT: Pan, James  
APPLICANT: Pitti, Robert M.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Smith, Victoria  
APPLICANT: Stone, Donna M.  
APPLICANT: Watanabe, Colin K.  
APPLICANT: Wood, William I.

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE TREATMENT OF TUMOR

FILE REFERENCE: P2931R1C1

CURRENT APPLICATION NUMBER: US/10/211,858

CURRENT FILING DATE: 2002-08-02

PRIOR APPLICATION NUMBER: 60/014699

PRIOR FILING DATE: 1996-04-01

PRIOR APPLICATION NUMBER: 60/026943

PRIOR FILING DATE: 1996-09-23

PRIOR APPLICATION NUMBER: 60/059121

PRIOR FILING DATE: 1997-07-17

PRIOR APPLICATION NUMBER: 60/059352

PRIOR FILING DATE: 1997-09-19

PRIOR APPLICATION NUMBER: 60/062037

PRIOR FILING DATE: 1997-10-10

PRIOR APPLICATION NUMBER: 60/063755

PRIOR FILING DATE: 1997-10-17

PRIOR APPLICATION NUMBER: 60/063045

PRIOR FILING DATE: 1997-10-24

PRIOR APPLICATION NUMBER: 60/063046

PRIOR FILING DATE: 1997-10-24

PRIOR APPLICATION NUMBER: 60/066511

PRIOR FILING DATE: 1997-11-24

PRIOR APPLICATION NUMBER: 60/066772

PRIOR FILING DATE: 1997-11-24

Remaining Prior Application data removed - See File Wrapper or PALM.

NUMBER OF SEQ ID NOS: 258

SEQ ID NO 27

LENGTH: 569

TYPE: DNA

ORGANISM: Homo sapiens

US-10-211-858-27

Query Match 13.9%; Score 78; DB 13; Length 569;

Best Local Similarity 100.0%; Pred. No. 2.5e-09;

Matches 78; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 474 GCGAGGACCGGGTATAGAGCCCTCGTGGCCTTCCCGGGCAGCCGAGGTTCCCGCGC 533

Db 1 GCGAGGACCGGGTATAGAGCCCTCGTGGCCTTCCCGGGCAGCCGAGGTTCCCGCGC 60

Qy 534 GCCCGAGCCCCCGCGCC 551

Db 61 GCCCGAGCCCCCGCGCC 78

RESULT 8

US-10-210-951-27

Sequence 27, Application US/10210951

Publication No. US20030170228A1

GENERAL INFORMATION:

APPLICANT: Ashkenazi, Avi J.

APPLICANT: Goddard, Audrey

APPLICANT: Godowski, Paul J.

APPLICANT: Gurney, Austin L.

APPLICANT: Hillan, Kenneth J.

APPLICANT: Marsters, Scot A.

APPLICANT: Pan, James

APPLICANT: Pitti, Robert M.

APPLICANT: Roy, Margaret Ann

APPLICANT: Smith, Victoria

APPLICANT: Stone, Donna M.

APPLICANT: Watanabe, Colin K.

APPLICANT: Wood, William I.

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE TREATMENT OF TUMOR

FILE REFERENCE: P2931R1C1

CURRENT APPLICATION NUMBER: US/10/210,951

CURRENT FILING DATE: 2002-08-02

PRIOR APPLICATION NUMBER: 60/014699

PRIOR FILING DATE: 1996-04-01

PRIOR APPLICATION NUMBER: 60/026943

PRIOR FILING DATE: 1996-09-23

PRIOR APPLICATION NUMBER: 60/059121

PRIOR FILING DATE: 1997-07-17

PRIOR APPLICATION NUMBER: 60/059352

PRIOR FILING DATE: 1997-09-19

PRIOR APPLICATION NUMBER: 60/062037

PRIOR FILING DATE: 1997-10-10

PRIOR APPLICATION NUMBER: 60/063755

PRIOR FILING DATE: 1997-10-17

PRIOR APPLICATION NUMBER: 60/063045

PRIOR FILING DATE: 1997-10-24

PRIOR APPLICATION NUMBER: 60/063046

PRIOR FILING DATE: 1997-10-24

PRIOR APPLICATION NUMBER: 60/066511

PRIOR FILING DATE: 1997-11-24

PRIOR APPLICATION NUMBER: 60/066772

PRIOR FILING DATE: 1997-11-24

Remaining Prior Application data removed - See File Wrapper or PALM.

NUMBER OF SEQ ID NOS: 258

SEQ ID NO 27

LENGTH: 569

TYPE: DNA

ORGANISM: Homo sapiens

US-10-210-951-27

Query Match 13.9%; Score 78; DB 15; Length 569;

Best Local Similarity 100.0%; Pred. No. 2.5e-09;

Matches 78; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 474 GCGAGGACCGGGTATAGAGCCCTCGTGGCCTTCCCGGGCAGCCGAGGTTCCCGCGC 533

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Qy 534 GCCCGAGCCCCCGCGCC 551

Db 61 GCCCGAGCCCCCGCGCC 78

RESULT 9

US-10-211-884-27

Sequence 27, Application US/10211884

Publication No. US20030175900A1

GENERAL INFORMATION:

APPLICANT: Ashkenazi, Avi J.

APPLICANT: Goddard, Audrey

APPLICANT: Godowski, Paul J.

APPLICANT: Gurney, Austin L.

APPLICANT: Hillan, Kenneth J.

APPLICANT: Marsters, Scot A.

APPLICANT: Pan, James

APPLICANT: Pitti, Robert M.

APPLICANT: Roy, Margaret Ann

APPLICANT: Smith, Victoria

APPLICANT: Stone, Donna M.

APPLICANT: Watanabe, Colin K.

APPLICANT: Wood, William I.

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE TREATMENT OF TUMOR

FILE REFERENCE: P2931R1C1

CURRENT APPLICATION NUMBER: US/10/211,884

CURRENT FILING DATE: 2002-08-02

PRIOR APPLICATION NUMBER: 60/014699

PRIOR FILING DATE: 1996-04-01

PRIOR APPLICATION NUMBER: 60/026943

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; PRIOR FILING DATE: 1997-11-24
; PRIOR APPLICATION NUMBER: 60/066772
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 258
; SEQ ID NO 27
; LENGTH: 569
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-211-884-27

Query Match      13.9%; Score 78; DB 15; Length 569;
Best Local Similarity 100.0%; Pred. No. 2.5e-09;
Matches 78; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 474 GCGAGGACCGGGTATAGAGCTCTGCGCTTCCCGGGCAGCCAGGTTCCCGCGC 533
Db 1 GCGAGGACCGGGTATAGAGCTCTGCGCTTCCCGGGCAGCCAGGTTCCCGCGC 60

QY 534 GCCCGAGCGCCCGCGCC 551
Db 61 GCCCGAGCGCCCGCGCC 78

RESULT 10
US-09-989-722-407
; Sequence 407, Application US/09989722
; Patent No. US20020072067A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kijavini, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William L.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2730P1C63
; CURRENT APPLICATION NUMBER: US/09/989,722
; CURRENT FILING DATE: 2001-11-19
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-12
; PRIOR APPLICATION NUMBER: 60/089105
; PRIOR FILING DATE: 1999-06-11
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; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-06-16
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PRIOR FILING DATE:	1998-06-16
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;; PRIOR FILING DATE: 1998-07-07  
;; PRIOR APPLICATION NUMBER: 60/091982  
;; PRIOR FILING DATE: 1998-07-07  
;; PRIOR APPLICATION NUMBER: 60/092182  
;; PRIOR FILING DATE: 1998-07-09

Query Match 13.9%; Score 78; DB 9; Length 570;

Best Local Similarity 100.0%; Pred. No. 2.5e-09;  
Matches 78; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 474 GCGAGGACCGGTTAAGAGCTCGTGGCTTCCCGGCGAGCGGAGGTTCCCGCGC 533  
Db 1 GCGAGGACCGGTTAAGAGCTCGTGGCTTCCCGGCGAGCGGAGGTTCCCGCGC 60  
QY 534 GCCCGAGCCCCCGCGCC 551  
Db 61 GCCCGAGCCCCCGCGCC 78

## RESULT 12

US-09-989-279-407

; Sequence 407, Application US/09989279

; Patent No. US20020072496A1

; GENERAL INFORMATION:

; APPLICANT: Ashkenazi, Avi J.

; APPLICANT: Baker, Kevin P.

; APPLICANT: Botstein, David

; APPLICANT: Desnoyers, Luc

; APPLICANT: Eaton, Dan L.

; APPLICANT: Ferrara, Napoleone

; APPLICANT: Fong, Sherman

; APPLICANT: Gerber, Hanspeter

; APPLICANT: Geritsen, Mary E.

; APPLICANT: Goddard, Audrey

; APPLICANT: Godowski, Paul J.

; APPLICANT: Grimaldi, J. Christopher

; APPLICANT: Gurney, Austin L.

; APPLICANT: Kljavin, Ivar J.

; APPLICANT: Napier, Mary A.

; APPLICANT: Pan, James

; APPLICANT: Paoni, Nicholas F.

; APPLICANT: Roy, Margaret Ann

; APPLICANT: Stewart, Timothy A.

; APPLICANT: Tumas, Daniel

; APPLICANT: Watanabe, Colin K.

; APPLICANT: Williams, P. Mickey

; APPLICANT: Wood, William I.

; APPLICANT: Zhang, Zemin

; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

; FILE REFERENCE: P2730P1C56

; CURRENT APPLICATION NUMBER: US/09/989,279

; PRIOR FILING DATE: 2001-11-19

; PRIOR APPLICATION NUMBER: 60/049787

; PRIOR FILING DATE: 1997-06-16

; PRIOR APPLICATION NUMBER: 60/062250

; PRIOR FILING DATE: 1997-10-17

; PRIOR APPLICATION NUMBER: 60/065186

; PRIOR FILING DATE: 1997-11-12

; PRIOR APPLICATION NUMBER: 60/065311

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;; PRIOR FILING DATE: 1998-07-07  
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;; PRIOR FILING DATE: 1998-07-07  
;; PRIOR APPLICATION NUMBER: 60/092182  
;; PRIOR FILING DATE: 1998-07-09

Query Match 13.9%; Score 78; DB 9; Length 570;  
Best Local Similarity 100.0%; Pred. No. 2.5e-09;  
Matches 78; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 474 GCGAGGACCGGGTATAGAGAGCTCTGGGCTTGGCCGGGACGCGCAGGTTCCCGCGC 533  
Db 1 GCGAGGACCGGGTATAGAGAGCTCTGGGCTTGGCCGGGACGCGCAGGTTCCCGCGC 60

QY 534 GCGGCGAGCCCCCGGCC 551  
Db 61 GCGGCGAGCCCCCGGCC 78

## RESULT 13

US-09-989-727-407  
; Sequence 407, Application US/09989727  
; Patent No. US20020072497A1

## GENERAL INFORMATION:

;; APPLICANT: Ashkenazi, Avi J.  
;; APPLICANT: Baker, Kevin P.  
;; APPLICANT: Botstein, David  
;; APPLICANT: Desnoyers, Luc  
;; APPLICANT: Eaton, Dan L.  
;; APPLICANT: Ferrara, Napoleone  
;; APPLICANT: Fong, Sherman  
;; APPLICANT: Gerber, Hanspeter  
;; APPLICANT: Gerritsen, Mary E.  
;; APPLICANT: Goddard, Audrey  
;; APPLICANT: Godowski, Paul J.  
;; APPLICANT: Grimaldi, J. Christopher  
;; APPLICANT: Gurney, Austin L.  
;; APPLICANT: Kijavini, Ivar J.  
;; APPLICANT: Napier, Mary A.  
;; APPLICANT: Pan, James  
;; APPLICANT: Paoni, Nicholas F.  
;; APPLICANT: Roy, Margaret Ann  
;; APPLICANT: Stewart, Timothy A.  
;; APPLICANT: Tumas, Daniel  
;; APPLICANT: Watanabe, Colin K.  
;; APPLICANT: Williams, P. Mickey  
;; APPLICANT: Wood, William I.  
;; APPLICANT: Zhang, Zemin  
;; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
;; FILE REFERENCE: P2730PIC65  
;; CURRENT APPLICATION NUMBER: US/09/989,727  
;; CURRENT FILING DATE: 2001-11-19  
;; PRIOR APPLICATION NUMBER: 60/049787  
;; PRIOR FILING DATE: 1997-06-16  
;; PRIOR APPLICATION NUMBER: 60/062250  
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/ PRIOR FILING DATE: 1998-07-09

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Db 1 GCGAGACCGGTATAGAGCTCTGCGCCCTGCGCGGCGACCGCAGGTTCCCGCGCC 60
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; Patent No. US20020103125A1
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; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
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; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
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; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin

TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2730P1C70
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CURRENT FILING DATE: 2001-11-20
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PRIOR FILING DATE: 1997-06-16
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PRIOR APPLICATION NUMBER: 60/075945
PRIOR FILING DATE: 1998-02-25
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; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi J.  
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; APPLICANT: Watanabe, Colin K.  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William I.  
; APPLICANT: Zhang, Zemin  
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; FILE REFERENCE: P2730PIC57  
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Search completed: June 6, 2004, 19:49:10  
Job time : 417 secs

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C	13	47.2	8.4	3937	3	US-08-586-165-8	Sequence 8, Appl
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C	19	46.8	8.3	4257	3	US-09-259-621A-1	Sequence 1, Appl
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C	21	46.6	8.3	932	1	US-08-458-568A-11	Sequence 11, Appl
C	22	46.6	8.3	932	1	US-08-458-912-1	Sequence 1, Appl
C	23	46.6	8.3	932	1	US-08-461-179-1	Sequence 1, Appl
C	24	46.6	8.3	932	1	US-08-459-254-1	Sequence 1, Appl
C	25	45.8	8.1	35060	3	US-08-439-255-1	Sequence 1, Appl
C	26	45.4	8.1	595	3	US-08-814-095-7	Sequence 7, Appl
C	27	45.4	8.1	595	3	US-08-483-533-4	Sequence 4, Appl
C	28	45.4	8.1	595	4	US-09-283-471A-4	Sequence 4, Appl

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; Sequence 1, Application PC/TUS9106532  
; GENERAL INFORMATION:  
; APPLICANT: Roizman, Bernard  
; TITLE OF INVENTION: Recombinant Herpes Simplex Viruses  
; TITLE OF INVENTION: Vaccines and Methods  
; NUMBER OF SEQUENCES: 8  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &  
; ADDRESSEE: Bicknell  
; STREET: Two First National Plaza Suite 2100  
; CITY: Chicago  
; STATE: Illinois  
; COUNTRY: USA  
; ZIP: 60603  
; COMPUTER READABLE FORM:  
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; FILING DATE: 19910910  
; CLASSIFICATION: 424  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Gruber, Lewis S.  
; REGISTRATION NUMBER: 30,060  
; REFERENCE/DOCKET NUMBER: 27373/8235  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 312/346-5750  
; TELEFAX: 312/984-9740  
; TELEX: 25-3856  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1335 base pairs  
; TYPE: NUCLEIC ACID  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
PCT-US91-06532-1

Query Match 8.8%; Score 49.4; DB 5; Length 1335;  
Best Local Similarity 48.0%; Pred. No. 0.056;  
Matches 169; Conservative 0; Mismatches 182; Indels 1; Gaps 1;

QY 169 GCGAGGAGTCCCTACACGAGGAGGAGTCCCTACCGCGCCCGAGCCCTGCGAGGGG 228  
Db 723 GGGCGAGAGCGCACCCGCGCGGGGTGCGCGGGGTGCGCGGGGTGCGGGGGT 664

QY 229 GCGGTGCGGTGAGAGCGCAAGAGGTGCGGGGCGGGGTGCGGTGCGGTGAGAGGAGG 288  
Db 663 GGTGCGGGGTGCGGGGGTTCGCGGGGTGCGGGGTGCGGGGTGCGGGGTGCGGGGT 604

QY 289 GCGCGGCGCTTCTCTCAGAGGCGCCCGAGCGCTGCGAGAGAGAGTCTCTCAGAGGCG 348  
Db 603 GCGGCGCCCTTCTCTCAGAGGCGCCCGAGCGCTGCGAGAGAGAGTCTCTCAGAGGCG 544

QY 349 GCGCAGGAGAGGGGCGAGGCTTCCAGGGCGCCCGCGCGAGCGAGAGTTCGAGGAG 408  
Db 543 GCGCAGGAGAGGGGCGAGGCGCGCGAGGCGCGAGGCGCGAGGCGCGAGGCGCGAGG 484

QY 409 GCGCAGGCGGTGAGCGGAGCGGGGCGAGGCTTCTCAGAGGCGCGGGC- GAGGCGGCGCT 467  
Db 483 GTTAGCCCCCGCCCCCGGGCGCGCGCGGGGTGAGGAGCGGGGGCGGGGGCGGGCGG 424

QY 468 GGAGGGGCGAGGAGCGGGGTATAGAGAGCTCTGTCGCTTGTCCCGGGGCGAGCG 519

Db 423 GGTGGCGCGGCGCTTGTGGCGCGCGCGCTCGGGCGGGGGGCTGTCCGGCAGTGG 372

RESULT 3  
US-09-289-48/c  
; Sequence 48, Application US/09616289  
; Patent No. 6632923  
; GENERAL INFORMATION:  
; APPLICANT: Lees, Ann M.  
; APPLICANT: Lees, Robert S.  
; APPLICANT: Law, Simon W.  
; APPLICANT: Artora, Anibal A.  
; TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING  
; TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING AND TREATING  
; TITLE OF INVENTION: ATHEROSCLEROSIS  
; FILE REFERENCE: 10797-004001  
; CURRENT APPLICATION NUMBER: US/09/616,289  
; CURRENT FILING DATE: 2000-07-14  
; PRIOR APPLICATION NUMBER: US 09/517,849  
; PRIOR FILING DATE: 2000-03-02  
; PRIOR APPLICATION NUMBER: US 08/979,608  
; PRIOR FILING DATE: 1997-11-26  
; PRIOR APPLICATION NUMBER: US 60/031,930  
; PRIOR FILING DATE: 1996-11-27  
; PRIOR APPLICATION NUMBER: US 60/048,547  
; PRIOR FILING DATE: 1997-06-03  
; NUMBER OF SEQ ID NOS: 53  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 48  
; LENGTH: 2561  
; TYPE: DNA  
; ORGANISM: Oryctolagus cuniculus  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (246)....(1895)  
US-09-616-289-48

Query Match 8.7%; Score 48.8; DB 4; Length 2561;  
Best Local Similarity 46.4%; Pred. No. 0.076;  
Matches 225; Conservative 0; Mismatches 258; Indels 2; Gaps 2;

QY 1 CGGCGGGAGGGCGCGGAGTGAGGCGCTGATCGCTCCCTCGCGCTCCACCTCCCGAGG 60  
Db 1084 CGGCGGTGAGGCGCGCGCGCGCGCTCTCTACCCCGAGGAGCGACATTTCCCGC 1025

QY 61 CGCAGAGGCGCCCAAGAGGACCCCGAGTCCCGAGAGTTCACCGGTCTGGGATCAGAGG 120  
Db 1024 AGGTCTACGGGCTGT 965

QY 121 CAGGACCGAGGAGCGCAGGAACTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCT 180  
Db 964 GGCTGTGCGCGCGCGCGGTGCGCGCGCGCGCGCTGTGTGTGTGTGTGTGTGTGTGT 905

QY 181 CCCTCACGCGAGGAGAGTCCCTCTACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 240  
Db 904 TGTGCG 846

QY 241 AGACCCGAAAGCGGAGGTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 300  
Db 845 GCG 786

QY 301 CTCTCTCAGAGGCG 360  
Db 785 GCGCAGGCG 727

QY 361 GCGCAGGCG 420  
Db 726 GCGCTGTGCG 667

QY 421 AGCGGAGCG 480  
Db 666 CGCGCAGCG 607



```

QY      481  CCGGG 485
      |||||
Db      606  CCGGG 602

RESULT 4
US-09-103-840A-2
; Sequence 2, Application US/09103840A
; Patent No. 6294328
; GENERAL INFORMATION:
; APPLICANT: FLEISCHMAN, Robert D.
; APPLICANT: WHITE, Owen R.
; APPLICANT: FRASER, Claire M.
; APPLICANT: VENTER, John C.
; TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
; TITLE OF INVENTION: TUBERCULOSIS
; FILE REFERENCE: 24366-20007.00
; CURRENT APPLICATION NUMBER: US/09/103,840A
; CURRENT FILING DATE: 1998-06-24
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 4403765
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
; FEATURE:
; OTHER INFORMATION: CDC 1551
; OTHER INFORMATION: "n" bases at various positions throughout the sequence
US-09-103-840A-2

```

```

RESULT 5
US-09-103-840A-1
; Sequence 1, Application US/09103840A
; Patent No. 6294328
; GENERAL INFORMATION:
; APPLICANT: FLEISCHMAN, Robert D.
; APPLICANT: WHITE, Owen R.
; APPLICANT: FRASER, Claire M.
; APPLICANT: VENTER, John C.
; TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
; TITLE OF INVENTION: TUBERCULOSIS
; FILE REFERENCE: 24366-20007.00
; CURRENT APPLICATION NUMBER: US/09/103.840A
; CURRENT FILING DATE: 1998-06-24
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO. 1
; LENGTH: 4411529
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
; OTHER INFORMATION: H37Rv
US-09-103-840A-1

Query Match      8.6%; Score 48.4; DB 3; Length 4411529;
Best Local Similarity 47.9%; Pred. No. 0.13;
Matches 237; Conservative 0; Mismatches 247; Indels 11; Gaps 3;

QY      1  CGCGCCGGGGAGCGCGCGGGAGTCGTCCTCGGCGGCTCCACCTCCCGAGG 60
db      838931  CGCGAGCGCGGGCGCGCGGGCGCTTCACCGACTCGCGCGGGGCGCGGTCGGTGGCGCGG 60

```

RESULT 6  
US-08-690-473-1/c  
Sequence 1, Application US/08690473  
; Patent No. 5876923  
; GENERAL INFORMATION:  
; APPLICANT: Leopardi, Rosario  
; APPLICANT: Reizman, Bernard  
; TITLE OF INVENTION: HERPES SIMPL  
; TITLE OF INVENTION: INHIBITOR O



Db	4348	CGCGGCTCTCGTGCCTGCGCGCGGCACGCGAGGTCCCGCGCGCATAGACACGCG	4407
QY	414	GGCGGTAGCGGAGCGGGCAGGGCTTTCTCAGAGCGCGGGCGAGCGCGCTGAGGG	473
Db	4408	CGTGGCGACGAAACCGCAGCTCGCGAGCACGCGCGAGGCGGGCGGCTCGCGCTGCG	4467
QY	474	GGGAGGACCGGGGTATAAAGACCTCTGTGGCTTTGCCGGGACGCCAGGTTCCCGCGCG	533
Db	4468	GCGGCGGCGGGAGACGGGGCCCGGGTCCCTCCGGCGCGGGGGGCTGGCGGGCGGG	4527
QY	534	GCCCCAGCCCCCGCGCCCGCGCG	557
Db	4528	CGCCGCGCAGCCCGCGGACGGCGG	4551

## RESULT 10

US-08-306-691B-14/c  
; Sequence 14, Application US/08306691B  
; Patent No. 5734039  
; GENERAL INFORMATION:  
; APPLICANT: Calabretta, Bruno  
; APPLICANT: Skorski, Tomasz  
; TITLE OF INVENTION: ANTISENSE  
; TITLE OF INVENTION: OLIGONUCLEOTIDES TARGETING COOPERATING ONCOGENES  
; NUMBER OF SEQUENCES: 55  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Seidel, Gonda, Lavorgna & Monaco, P.C.  
; STREET: Two Penn Center, Suite 1800  
; CITY: Philadelphia  
; STATE: Pennsylvania  
; COUNTRY: U.S.A.  
; ZIP: 19102

## COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 3.50 inch, 720 Kb

COMPUTER: IBM PS/2

OPERATING SYSTEM: MS-DOS

SOFTWARE: WordPerfect 5.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/306,691B

FILING DATE: September 15, 1994

CLASSIFICATION: 514

PRIOR APPLICATION DATA:

APPLICATION NUMBER:

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Monaco, Daniel A.

REGISTRATION NUMBER: 30,480

REFERENCE/DOCKET NUMBER: 8321-8

TELECOMMUNICATION INFORMATION:

TELEPHONE: (215) 568-8383

TELEFAX: (215) 568-5549

TELEX: No. 5734039e

INFORMATION FOR SEQ ID NO: 14:

SEQUENCE CHARACTERISTICS:

LENGTH: 6453 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

US-08-306-691B-14

Query Match 8.4%; Score 47.4; DB 1; Length 6453;

Best Local Similarity 46.5%; Pred. No. 0.15;

Matches 255; Conservative 0; Mismatches 287; Indels 6; Gaps 3;

Qy	9	GAGCGCGCGGAGTGAGGCGCTGATCGTCCCTGGCGCTCCACCTCCCGGCGGAGG	68
Db	883	GACGCCCGCGGTGTGAGGCGCGCGGCGCGGAGGCTCCCGGCTAGCGCGGTGGGACC	824
Qy	69	GCGGCCACAGAGACCCCGAGTGGCGGAGTTGCCAGCGTCTGGGATCAGAGCGAGGACC	128
Db	823	GTGCCCGACGCGGAGGCCACGCGTGGGCGCGCGGATTCGCCGAGGCGCCCGAGGAGGAGG	764
Qy	129	AGGAGCGCAGGAACCTGCGCCCGCCCGTCCCTGGCGCGGAGGAGGAGTCCCTCACC	188
Db	763	CCCCCGCCCGGAGCGAGCCCGCGCTTACCGCGCGCGCGCCCGCGCGCGCGCGCGCG	705
Qy	189	NGAGGAGAGTCTCCCTACCCCGCCCGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG	248
Db	704	CCACCCACCGCGCGCGCGCGCGCTTACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG	645
Qy	249	AAGCAGAGTCCGGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG	308
Db	644	CCGGCGGTAATTCCTGCGCGCTTGGGCGGCGGAGGAGGCGGCGGCGGCGGCGGCGGCGG	585
Qy	309	GAGGCGCCCGCGGCTGCCAGAGGAGTCTCCGAGGCGCGCGGCGGCGGCGGCGGCGGCGG	368
Db	584	GCATCACCGTTACAGGC--CGGACTCCCCCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG	527

Qy	369	GCTTCCACAGGCGCGCGCGCGAGGAAAGTTGGCCAGGCGACGCGCGTGGAGGAGC	428
Db	526	CGCGGCGCGGCGCGGCGCGGCTTCGCCCGCGCATGGCC--TCCGTCCGCGGCGG	470
Qy	429	GGGCGAGGCGCTTCTCAGGAGCGCGGCGGAGCGCGCGCTGGAGGCGGAGACCGGTTAT	488
Db	469	GTGCGGCTCGGTTTGGCGGCGCAGGCGACGCGGCGGAGACTCGGCGGCGCTTGGCAC	410
Qy	489	AAGAAAGCTCGTGGCGCTTGGCGGCGGCGGCGGAGCGGAGTTCCCGCGGCGGCGGCGG	548
Db	409	GCCCCGCGCGCGCGCGCTTCCTCTGCCAGGCGCGGCGCTTACCATTTGGTGGCGCGCATCG	350
Qy	549	GCCCGGCGC 556	
Db	349	GCCCCGCGC 342	

## RESULT 11

US-09-209-668-10/c

; Sequence 10, Application US/09209668A

; Patent No. 6114517

; GENERAL INFORMATION:

; APPLICANT: Monia, Brett P.

; APPLICANT: Xu, Xiaoxing S.

; TITLE OF INVENTION: METHODS OF MODULATING TUMOR NECROSIS FACTOR

; TITLE OF INVENTION: alpha-INDUCED EXPRESSION OF CELL ADHESION MOLECULES

; FILE REFERENCE: ISPH-0336

; CURRENT APPLICATION NUMBER: US/09/209,668A

; CURRENT FILING DATE: 1998-12-10

; NUMBER OF SEQ ID NOS: 25

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 10

; LENGTH: 6453

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: CDS

; LOCATION: (1664)..(1774)

; FEATURE:

; NAME/KEY: CDS

; LOCATION: (2042)..(2220)

; FEATURE:

; NAME/KEY: CDS

; LOCATION: (2374)..(2533)

; FEATURE:

; NAME/KEY: CDS

; LOCATION: (3211)..(3350)

; PUBLICATION INFORMATION:

; DATABASE ACCESSION NUMBER: V00574/Genbank

; DATABASE ENTRY DATE: 1991-01-03

US-09-209-668-10

Query Match 8.4%; Score 47.4; DB 3; Length 6453;

Best Local Similarity 46.5%; Pred. No. 0.15;

Matches 255; Conservative 0; Mismatches 287; Indels 6; Gaps 3;

Qy	9	GAGCGGCGCGGAGTGAGGCGCTGATCGTCCCTGGCGCTCCACCTCCCGGCGGAGG	68
Db	883	GACGCCCGCGGTGTGAGGCGCGCGGCGCGGAGGCTCCCGGCTAGCGCGGTGGGACC	824
Qy	69	GCGGCCACAGAGACCCCGAGTGGCGGCGGAGGCTTGGGATCAGAGGCGGAGGACC	128
Db	823	GTGCCCGACGCGGAGGCCACGCGTGGGCGCGGAGTTCGCCGAGGCGCCCGAGGAGG	764
Qy	129	AGGAGCGCAGGAACCTGCGCCCGCCCGTCCCTGGCGCGGAGGAGGAGTCCCTCACC	188
Db	763	CCCCCGCCCGGAGCGAGCCCGCGCTACCTGTGCCGCGGCGCGCGCGCGCGCGCG	705
Qy	189	NGAGGAGAGTCTCCCTACCCCGCCCGAGCGCTCAGAGGCGGCGGCGGCGGCGGCGG	248
Db	704	CCACCCACCGCGCGCGCGCGCTTACGCGCGCGCGCGCGCGCGCGCGCGCGCGCG	645



Db 395 GTCCCGAGCCCGCGCGTCCCGGACGTCGCTCCCGCGGCGCGCCCTCCCGC 336  
 QY 327 CAAGAGGAAGTCTCGAGCCCGGGCAG--GGAAGGGGCGACGGGCTTCCAGGGCGCGC 384  
 Db 335 TTCCGGGAGGGCTGTGCGCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 276  
 QY 385 CGCGCGCAGCAGGAAGTTGGCCAGGCGACGCGCGGTGAGCGGAGCGGCGAGGCTTTCTCA 444  
 Db 275 TGTCCCGCGGCGGAGCAGCAGCAGGAGACGCGCGCGGTGACCGACAGCAGGAAGCA 216  
 QY 445 GGAGCGCGCGCGCGCGCGCTGGAGGGCGGAGACGGGTATAAGAGCCTCGTGCC 504  
 Db 215 GCGTTCGCGAGCCCGCAGCAGAGCTGCTCATGTGCGGCGCCCGCGCGCGCGCG 156  
 QY 505 TTGCGCGGCGAGCGCGAGTTCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 558  
 Db 155 CTGCGCGCGCAGCTCATGCGCCCGCGGAGCGCGCGGAGCGTTCCTCCCGCGG 102

## RESULT 14

US-08-232-463-14/c

; Sequence 14, Application US/08232463

; Patent No. 5670367

; GENERAL INFORMATION:

; APPLICANT: DORNER, F.

; APPLICANT: SCHEIFLINGER, F.

; APPLICANT: FALKNER, F. G.

; TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS

; NUMBER OF SEQUENCES: 52

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Foley &amp; Lardner

; STREET: 1800 Diagonal Road, Suite 500

; CITY: Alexandria

; STATE: VA

; COUNTRY: USA

; ZIP: 22313-0299

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent in Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/232,463

; FILING DATE:

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US/07/935,313

; FILING DATE:

; APPLICATION NUMBER: EP 91 114 300.6

; FILING DATE: 26-AUG-1991

; ATTORNEY/AGENT INFORMATION:

; NAME: BENT, Stephen A.

; REGISTRATION NUMBER: 29,768

; REFERENCE/DOCKET NUMBER: 30472/114 INMU

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (703)836-9300

; TELEFAX: (703)683-4109

; TELEX: 899149

; INFORMATION FOR SEQ ID NO: 14:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 7218 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; IMMEDIATE SOURCE:

; CLONE: pTZgpt-F15

US-08-232-463-14

Query Match

Best Local Similarity 8.4%; Score 47.2; DB 1; Length 7218;

Matches 13; Conservative 171; Mismatches 114; Indels 0; Gaps 0;

QY 223 AGGGGGCGCGTGGGTGAGCCGCAAGAGTGGCGCGCGGTGGCGCTCGCGGA 282  
 Db 1339 RRR 1280  
 QY 283 GACAAAGCCCGGCTGCTCTCTCAGAGGCCCGCAGCGCTGCCAAGAGGAAAGTTCG 342  
 Db 1279 RRR 1220  
 QY 343 AGGCCCGGCGAGGAAGGGGCGCGGCTTCCAGGGCCCGCGCGCGCAGCAAGTT 402  
 Db 1219 RRR 1160  
 QY 403 GCGCAGGCGACGCGCGTACGCGAGCGGCGAGGCGCTTCTCAGAGCGCGCGCGCGCG 462  
 Db 1159 RRR 1100  
 QY 463 CGCTGAGGGCGGAGGACCGGTATAGAGCCTGTGGCTTGGCGCGCGCGCGCG 520  
 Db 1099 RRR 1042

## RESULT 15

US-09-616-289-45

; Sequence 45, Application US/09616289

; Patent No. 6632923

; GENERAL INFORMATION:

; APPLICANT: Lees, Ann M.

; APPLICANT: Lees, Robert S.

; APPLICANT: Law, Simon W.

; APPLICANT: Arjona, Anibal A.

; TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING

; TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING AND TREATING

; TITLE OF INVENTION: ATHEROSCLEROSIS

; FILE REFERENCE: 10797-004001

; CURRENT APPLICATION NUMBER: US/09/616,289

; CURRENT FILING DATE: 2000-07-14

; PRIOR APPLICATION NUMBER: US 09/517,849

; PRIOR FILING DATE: 2000-03-02

; PRIOR APPLICATION NUMBER: US 08/979,608

; PRIOR FILING DATE: 1997-11-26

; PRIOR APPLICATION NUMBER: US 60/031,930

; PRIOR FILING DATE: 1996-11-27

; PRIOR APPLICATION NUMBER: US 60/048,547

; PRIOR FILING DATE: 1997-06-03

; NUMBER OF SEQ ID NOS: 53

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 45

; LENGTH: 1614

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: CDS

; LOCATION: (1)...(1614)

US-09-616-289-45

Query Match

Best Local Similarity 8.3%; Score 47; DB 4; Length 1614;

Matches 257; Conservative 0; Mismatches 286; Indels 9; Gaps 3;

QY 1 CGGCGGGGAGGGCGCGGAGTGAGCGCTGATGTCCTTGGCGCGCTTCACTCCCGAGG 60  
 Db 306 CCGGCGCGGAGCACCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 365  
 QY 61 CGCAGAGGCGCCACGAGGACCCCGAGTCCCGAGTTCGCGGTCGCGATCAGAG 120  
 Db 366 CG 425  
 QY 121 CAGGGACGAGGAGCCAGAGAACTGCGCGCGCGCGCGCGCGCGCGCGCGCG 180  
 Db 426 CG 485  
 QY 181 CCTTCAACGAGGAGAGCTCCCTCTCAACCGCGCGCGCGCGCGCGCGCGCG 233

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Db 486 TGGCCCCCGGCGACCGGGCCCCCGCGGCGAGCGGGCCGCGCCCCCTGGCCCGCGCGCGGC 545
QY 234 TGGGTCAGACCCGAAAGCGAAGTGGGCGCGGGCTGGGCTCGGGGAGACAAAGGCCG 293
Db 546 CGGCGCAGCGCTCCCCCGCGGTGGCGCCCCCGCGCGCGCGCCCCCGCGCC 605
QY 294 GGCCTGCTCTCTCAGAGGCCCCCAGCGCTGCGAAGAGGAAGTCTCTGAGGCCCCGGGA 353
Db 606 CGCCGTGCGCGCCCGGAGCGCGCTGCGCGCGCGCCACAGCCCGCGCGCGCCACA 665
QY 354 GGGAGGGGGCAGCGGCTTCCAGGGCCCCCGCGCGCGAGCGAAGTTGGCCAGGGCAC 413
Db 666 GCAGCAGCGCGCCCGCGCGCGAGCCACAGCCCGCGCGCGAGGGGGCGCGTGGGGC 725
QY 414 GGCCTGTAGCGGAGCGGGCGAGGGCTTTCTCAGAGCGCGGGCGAGCGCGCGCTGGAGGG 473
Db 726 CGGCG-GCGCGCGCGCGCGCTGAGCCTGCGGGAAGTCTGTGCTACTCTCGGGGGCAGCG 784
QY 474 GCGAGGACCG-GGTATAAGAGCTCTGTGCTTGTGCGCGCGCGAGCGCGAGGTTCCCGCG 532
Db 785 GCGGCGCGCGCGCTCGCTTAACCGCGCGCGCTGAGGGGCTGCTGAGAGGAGGGCG 844
QY 533 CGCCCCGAGGCC 544
Db 845 CGGCTCGAGGCC 856
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Search completed: June 6, 2004, 18:43:53  
Job time : 99 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 6, 2004, 16:39:00 ; Search time 2620 Seconds  
(without alignments)  
6416.949 Million cell updates/sec

Title: SEQ19PLUS12

Perfect score: 563

Sequence: 1 cggcggggaggcggcgggg.....ccgcggcggcggcggagg 563

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:\*

1: em\_estba:\*

2: em\_esthum:\*

3: em\_estin:\*

4: em\_estmu:\*

5: em\_estov:\*

6: em\_estpl:\*

7: em\_estro:\*

8: em\_hic:\*

9: gb\_est1:\*

10: gb\_est2:\*

11: gb\_hic:\*

12: gb\_est3:\*

13: gb\_est4:\*

14: gb\_est5:\*

15: em\_estfun:\*

16: em\_estom:\*

17: em\_gss\_hum:\*

18: em\_gss\_inv:\*

19: em\_gss\_pln:\*

20: em\_gss\_vrt:\*

21: em\_gss\_fun:\*

22: em\_gss\_nam:\*

23: em\_gss\_mus:\*

24: em\_gss\_pro:\*

25: em\_gss\_rod:\*

26: em\_gss\_phg:\*

27: em\_gss\_vrl:\*

28: gb\_gss1:\*

29: gb\_gss2:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	88.4	15.7	982	13	BX415111 BX415111
2	82.2	14.6	982	13	BX415111 BX415111
3	81.6	14.5	1203	29	CNS015Y4
4	81.2	14.4	935	29	CNS06XX

#### ALIGNMENTS

RESULT 1  
BX415111/c  
LOCUS  
DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT  
FEATURES

982 bp mRNA linear EST 15-MAY-2003  
BX415111 Homo sapiens THYMUS Homo sapiens cDNA clone CS0CAP004YI20  
5-PRIME, mRNA sequence.

1 GI:30765470  
EST.

Homo sapiens (human)

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

1 (bases 1 to 982)

Li.W.B., Gruber,C., Jessee,J. and Polayes,D.

Full-length cDNA libraries and normalization

Unpublished (2001)

Contact: Genoscope

Genoscope - Centre National de Sequencage

BP 191 91006 EVRY cedex - France

Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr

Library was constructed by Life Technologies, a division of

Invitrogen. Contact : Feng Liang Email : fliang@lifetech.com URL :

http://fulllength.invitrogen.com/Invitrogen Corporation 1600

Faraday Avenue Genoscope sequence ID : CS0CAP004BE10QPL1.

Location/Qualifiers

1..982

/organism="Homo sapiens"

AG032885 Pan trogl  
BG852363 102403AA0  
BM547577 AGENCOURT  
AL053013 Drosophil  
AL108460 Drosophil  
AL066742 Drosophil  
CG757066 P052-2-A0  
BG681076 AGENCOURT  
BG809572 mgct001xa  
BG786331 SEADMC006  
AG043499 Pan trogl  
CK210297 FGAS02209  
AL108162 Drosophil  
AL539262 AL539262  
AL099352 Drosophil  
AL108855 Drosophil  
BU502934 AGENCOURT  
BX405071 BX405071  
CF217719 AGENCOURT  
BG844318 1024005H1  
AG152796 Pan trogl  
AG080291 Pan trogl  
AG126333 Pan trogl  
BM562099 AGENCOURT  
BX442207 BX442207  
B2690979 M037E05 G  
BO721449 AGENCOURT  
BX415926 BX415926  
AZ187356 SP\_1008 B  
AL098787 Drosophil  
AG161988 Pan trogl  
BX405071 BX405071  
BM909809 AGENCOURT  
AG052690 Pan trogl  
AG078581 Pan trogl  
AL053013 Drosophil  
AL063912 Drosophil  
AG154144 Pan trogl  
AL066742 Drosophil  
B2051933 jnr56A04.  
BQ434910 AGENCOURT



double-strand cDNA was digested with Not I and cloned into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library was not normalized.

ORIGIN

Library was not normalized.

one parameter is vector:

Best Local Similarity 32.5%; Pred. No. 0.00022; Indels 0; Gaps 0;  
Matches 150; Conservative 100; Mismatches 211;

QY	100	GCCACGCTCGGATCAGAGGCAGGACCAGGAGCCAGAACTCGCGCCGCCCCCCCCC	159
Db	129	SSSGVGVYSSSSSSSSSSSSSSCCCCYCVGGGGGGSCCSVSVSGSCCCSSSCG	188
QY	160	TGCCTTGGCGCAGGAAGCTCCCTCACNCGAGGGAAGTCCTCCCTCACCGGCCACGCC	219
Db	189	KCCCGKCCCCCCCCGGGGGGCCCCSSSSSCCCSCSsccccccccc	248
QY	220	TGCAGGGGGCGTGTTGGGTACAGCCGAAAGCAAGGTGCGGGCCGGGTGGGCTCGC	279
Db	249	CCCCCCCCCCCCGGGGCCCCCSCCSSCCGSSSSCSGSCSGSSCCGSGGGGG	308
QY	280	GGAGACAAGGCGGGCTTCCTCTCTCAGAGGGCCCCAGCGCTGCGAAGAGAAATCC	339
Db	309	GGSSSCSGSGGGSSSSSSSGSGSCCGGGGGSSCSSSGGCCSGSCSCSGGGSSSS	368
QY	340	TCGAGCCCCGGCAGGAAGGGGCACGGCTTCCAGGGCCCGCCGGCCGACAGCAA	399
Db	369	CSCGSCSSSGGGSSSGGGSSSGGGSMSSSSSGCCCCCGCCSCGGGGSSGS	428
QY	400	GTTGGCAGGCACGCCCTGTGACGAGCGGGCAGGGCTTCTCAGAGGCGCGGGCAGG	459
Db	429	CGSGGGSGVGGGSSCGCCCGSCSGSGSGGGGGSSCCSGGGGGCCCCGGGGSCGGG	488
QY	460	CGGGCGCTGAGGGCGAGCAGCGGTATAGAAGACTCGTGGCTTGCCTCCGGCGAGCCG	519
Db	489	GGGCGSSCGSSGGGGGGGGGGSSCGSCCGGCCCMGGGCCCCGCCCCCCCC	548
QY	520	CAGGTTCCCGCGCCCCCGAGCCCCCGCCCGCCGGCGGGG	560
Db	549	GCCCCACAGAGGASCCARACCSGAVAGSCGACACCGG	589

Db 549 GCCCCACAGACGGASCCARACCSGAVAGSCSGACACCGG 589

LOCUS	CNS015Y4	1203 bp	DNA	linear	GSS 26-JUL-1999			
DEFINITION	Drosophila melanogaster genome survey sequence 17 end of BAC BACN15E10 of DrosBAC library from Drosophila melanogaster (fruit fly), genomic survey sequence.							
ACCESSION	AL106054							
VERSION	AL106054.1	GI:5619805						
KEYWORDS								
SOURCE	GSS							
ORGANISM	Drosophila melanogaster (fruit fly)							
	Drosophila melanogaster							
	Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.							
REFERENCE	1. (bases 1 to 1203)							
AUTHORS	Genoscope.							
TITLE	Direct Submission							
JOURNAL	Submitted (23-JUL-1999) Genoscope -- Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)							
COMMENT	Determination of this BAC-end sequence was carried out as part of a							

collaboration with the European Drosophila Genome Project (EDGP) - <http://www.edgp.ebi.ac.uk> -- this Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CEPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector pBelobAC11.

# Location/Qualifiers

```

1. .1203
/organism="Drosophila melanogaster"
/mol_type="genomic DNA"
/db_xref="taxon:7227"
/clone="BACN15E10"
/clone_lib="DrosBAC"
/plasmid="pBelobAC11"
/note="end : T7"

```

## ORIGIN

```

Query Match      14.5%; Score 81.6; DB 29; Length 1203;
Best Local Similarity 34.5%; Pred. No. 0.00029;
Matches 153; Conservative 88; Mismatches 203; Indels 0; Gaps 0;

QY 120 GAGGACACAGGAGCAGGAATGCGCCCGCCCGCCCTGCGCGCGGGAAGC 179
   |||: : : : : : : : : : : : : : : : : : : : : : : : :
Db 677 GSGSCSSSCSSSCSCSCSCSCSCSCSCSCSCSCSCSCSCSCSCSC 736

QY 180 TCCTCACNAGAGGAGCTCCCTACCCCGGCCAGCCCTGCGAGGGGCGTGGGT 239
   |||: : : : : : : : : : : : : : : : : : : : : : : : :
Db 737 GGGSGGGGCGCGCGCYCCCGCCCGCCCGCCCGCCCGCCCGCCCGCC 796

QY 240 CAGACCGCAAGCAGAGTCGGGCGCGGCTGGGCTCGCGAGACAAAGCCGGCTG 299
   |||: : : : : : : : : : : : : : : : : : : : : : : : :
Db 797 GGGCGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 856

QY 300 CTCTCTCTCAGAGGCGCCCGCAGCGCTGCGAAGAGAGTCTCTCAGGCGCC 359
   |||: : : : : : : : : : : : : : : : : : : : : : : : :
Db 857 GCGCGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 916

QY 360 GGGGACAGGCTTCCAGAGGCGCCCGCGCGCAGAGGAGTTGGCAGGCGACGCG 419
   |||: : : : : : : : : : : : : : : : : : : : : : : : :
Db 917 GGGGGMVSGGGGVVGGVVGVMVGGGSMGGMVGMVGGGGMVGGGGMVSSV 976

QY 420 GAGCGAGGGGCGAGGCTTCTCAGAGCGCGGGCGAGCGCGCTGAGGGGGGAGG 479
   |||: : : : : : : : : : : : : : : : : : : : : : : : :
Db 977 SSGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 1036

QY 480 ACCGGGTATAAGAGGCTCTGTGCTTTCGCGGCGAGCGCGAGTTCCCGCGCC 539
   |||: : : : : : : : : : : : : : : : : : : : : : : : :
Db 1037 GGGSSSSGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 1096

QY 540 AGCCCCCGCGCGCGCGGGGAGG 563
   |||: : : : : : : : : : : : : : : : : : : : : : : : :
Db 1097 CSCCCCGSCCCSCSSSGGGGGG 1120

```

## RESULT 4

```

CNS006XK
LOCUS
DEFINITION
Drosophila melanogaster genome survey sequence T7 end of BAC #
BAC14N09 of RPI-98 library from Drosophila melanogaster (fruit
fly), genomic survey sequence.
AL066051
AL066051.1 GI:4945019
GSS.
Drosophila melanogaster (fruit fly)
Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 935)
Genoscope.
Direct Submission
Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :

```

## ACCESSION

## VERSION

## KEYWORDS

## SOURCE

## ORGANISM

## REFERENCE

## AUTHORS

## TITLE

## JOURNAL

## COMMENT

BP 191 91006 EVRY cedex - FRANCE (E-mail : [seqref@genoscope.cns.fr](mailto:seqref@genoscope.cns.fr))  
 - Web : [www.genoscope.cns.fr](http://www.genoscope.cns.fr)  
 Determination of this BAC-end sequence was carried out as part of a  
 collaboration with the Berkeley Drosophila Genome Project (BDGP).  
 The BDGP is constructing a physical map of the Drosophila  
 melanogaster genome using these BACs. For further information  
 please see <http://www.fruitfly.org> The BDGP Drosophila  
 melanogaster BAC library was prepared by Kazutoyo Osoegawa and  
 Aaron Mammoler in Pieter de Jong's laboratory in the Department of  
 Cancer Genetics at the Roswell Park Cancer Institute in Buffalo,  
 NY. The library is named RPI-98 and was constructed by partial  
 EcoRI digestion of Drosophila DNA provided by the BDGP from the  
 isogenic strain Y2; cn bw sp, the same strain used for the BDGP's  
 P1 and EST libraries. A more detailed description of the library  
 and how to order individual BAC clones, the entire library, or  
 filters for hybridization from the BACPAC Resource Center can be  
 found at [http://bacpac.med.buffalo.edu/drosophila\\_bac.htm](http://bacpac.med.buffalo.edu/drosophila_bac.htm).

## FEATURES

## source

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1. .935
/organism="Drosophila melanogaster"
/mol_type="genomic DNA"
/db_xref="taxon:7227"
/clone="BAC14N09"
/clone_lib="RPI-98"
/note="end : T7"

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## ORIGIN

```

Query Match      14.4%; Score 81.2; DB 29; Length 935;
Best Local Similarity 32.9%; Pred. No. 0.00032;
Matches 130; Conservative 92; Mismatches 173; Indels 0; Gaps 0;

QY 145 CGCGCGCCCGCCCTGCGCGGAGGAGTCTCCACNAGGAGGAGTCCCT 204
   |||: : : : : : : : : : : : : : : : : : : : : : : : :
Db 538 CCGCGTCCGCTCKWCTGCTGCGCGCGCTSCSSSSCCSBBYSVTCSTCTCT 597

QY 205 CACCGCGCCAGCCCTGCGAGGGGGCGCGTGGGTGAGACCGAAGCGAGTGGG 264
   |||: : : : : : : : : : : : : : : : : : : : : : : : :
Db 598 SGGCTGSGCTCGCGGGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 657

QY 265 CGGGGTGGCGCTCGGGGACAAAGCGCGCGCGCTCTCTCAGAGGCGCCG 324
   |||: : : : : : : : : : : : : : : : : : : : : : : : :
Db 658 CGSSSGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 717

QY 325 GCGAAGAGAGAGTCTCTGAGGCGCGCGCGAGGAGGAGGAGGAGGAGG 384
   |||: : : : : : : : : : : : : : : : : : : : : : : : :
Db 718 CSCSSCGSGSGSGSGSGSGSGSGSGSGSGSGSGSGSGSGSGSGSGSG 777

QY 385 CGGCGCGCAGAGAGTTGGCCAGGGGCGCGCGTGGAGCGAGCGGGGAGGGCT 444
   |||: : : : : : : : : : : : : : : : : : : : : : : : :
Db 778 CSGCCGCGSGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 837

QY 445 GAGAGCGCGCGGAGCGCGCTGGAGGGGCGAGGACCGGGGTATAGAGCC 504
   |||: : : : : : : : : : : : : : : : : : : : : : : : :
Db 838 SGGGCGCGSSCGCGCGGGGCGCGGGGCGCGGGGCGCGGGGCGGGG 897

QY 505 TTGCGCGGCGAGCGCGAGGTTCCCGCGCGCGCGCGCGCGCGCGCG 539
   |||: : : : : : : : : : : : : : : : : : : : : : : : :
Db 898 SCGSGGGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 932

```

## RESULT 5

## LOCUS

## AG032885

## DEFINITION

## AG032885

## ACCESSION

## AG032885.1

## VERSION

## AG032885.1

## KEYWORDS

## SOURCE

## Pan troglodytes (chimpanzee)

## ORGANISM

## Pan troglodytes

## Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

## Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.

## 1

## REFERENCE

## AUTHORS

## Fujiyama,A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T.,

AG032885 1313 bp DNA linear GSS 01-NOV-2001.  
 Pan troglodytes DNA, clone: PTB-007M05.F, genomic survey sequence.

AG032885  
 AG032885.1 GI:16559758  
 GSS.

Pan troglodytes (chimpanzee)  
 Pan troglodytes  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.  
 1

REFERENCE  
 AUTHORS  
 Fujiyama,A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T.,



QY 301 CTCCTCTCAG--AGGGCCCAAGCGCCTTCCCAAGAGGAAGTCTCTGAGCCCGGGCAGGGAA 358  
 Db 768 CGGGGNGCGCCGCGGNGNCNCCGCGGGGGCGCGCGGGCCNGCGCGGGGCGCGGGGGGGGCG 709  
 QY 359 GGGGGCAGGGCTTCCAGAGGCCCGCGCGCGCAGCAGGAAGTTGGCCAGGGCACGGCCG 418  
 Db 708 GCGGCGGGCGNGGGGGGGGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 649  
 QY 419 TGAGCGGAGGGGGCAGGGCTTCTTCAGAGCGCGGGCGAGCGCGCGCTCGAGGGGGCGAG 478  
 Db 648 CGCCCGCGGGGGGNGCCGCGCGCNCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 599  
 QY 479 GACCGGTATAAGAGCCTCTGTGGCCCTTCCCGCGCAGCGCAGGTTCCCGCGCGCGCCC 538  
 Db 588 GGGCGGGGGCGCGCGCGCC-GGGGCGGGCGCGCGCGGGGGGGCGGGGGCGGGGGGCG 530  
 QY 539 GAGCCCCCGCGCGCGCGGGGAGG 563  
 Db 529 CGGGCGGGCGCGCGCGCGCGCGCG 505

RESULT 7  
 BM547577/c  
 LOCUS  
 DEFINITION  
 AGENCOURT\_6507057 NIH\_MGC\_124 Homo sapiens cDNA clone IMAGE:5727629  
 5', mRNA sequence.  
 BM547577  
 BM547577.1 GI:18781461  
 EST.  
 SOURCE  
 Homo sapiens (human)  
 ORGANISM  
 Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 1 (bases 1 to 1284)  
 NIH-MGC http://mgi.nci.nih.gov/  
 National Institutes of Health, Mammalian Gene Collection (MGC)  
 Unpublished (1999)  
 Contact: Robert Strausberg, Ph.D.  
 Email: cgapbs@mail.nih.gov  
 Tissue Procurement: Invitrogen  
 CDNA Library Preparation: Life Technologies, Inc.  
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
 DNA Sequencing by: Agencourt Bioscience Corporation  
 Clone Distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:  
 http://image.llnl.gov  
 Plate: LLNL2722 row: a column: 06  
 High quality sequence stop: 249.  
 Location/Qualifiers  
 1..1284  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:5727629"  
 /tissue\_type="hippocampus"  
 /lab\_host="PH108"  
 /clone\_lib="NIH MGC 124"  
 /note="Organ: brain; Vector: pCMV-SPORT6; Site\_1: EcoRV  
 (destroyed); Site\_2: NotI; RNA source male hippocampus,  
 age 27. Library is oligo-dT primed and directionally  
 cloned (EcoRV site is destroyed upon cloning). Average  
 insert size 1.4 kb, insert size range 0.9-4 kb. Library is  
 normalized and enriched for full-length clones and was  
 constructed by C. Gruber (Invitrogen). Research Genetics  
 tracking code 012."

FEATURES  
 source  
 13.7%; Score 77.4; DB 12; Length 1284;  
 Query Match  
 Best Local Similarity 45.6%; Pred. No. 0.0015;  
 Matches 259; Conservative 0; Mismatches 303; Indels 6; Gaps 1;  
 1 CGGCCGGGAGGGCGGGAGTGGAGCTGATCGCTCCCTGGCGCTCCACTCCCGAGG 60

ORIGIN

Db 1219 CGNCCGCGNGNCCNNNGCGGGCGCGCNCNCCCGGGCGGGCGCGCGCCCGCCCGCCG 1160  
 QY 61 CGCAGAAGCGCCGCCACGAGGACCCCGAGTGCCCGAGAGTTGCGCACGGTCTCGGATCAGAG 120  
 Db 1159 CGCGCGGGCG 1100  
 QY 121 CAGGGACCAAG-----GAGCCAGGAACCTGCGCGCGCCCGCGCGCGCGCGCGCGCG 174  
 Db 1099 CGGGCGCNCGCGGGGGCG 1040  
 QY 175 GAAGTCTCTCAACNAGAGGAAGTCTCCCTCAACCCCGCGCGCGCGCGCGCGCGCGCG 234  
 Db 1039 GCG 980  
 QY 235 GGGGTGAGACCGCAAGCGAAGTGGGGCGGGGTGGGCTTCGCGGAGACAAAGGCCGG 294  
 Db 979 GCGNNNGCG 920  
 QY 295 GCCTGCTCTCTCAGAGGGCGCCCGAGCGCTGCTCAAGAGGAAGTCTCTCAGAGGCCCGGGCAG 354  
 Db 919 CG 860  
 QY 355 GGAAGGGGCGACGGGCTTCCCAAGGGCGCCCGCGCGCGCGCGCGCGCGCGCGCGCGCG 414  
 Db 859 GGGGGCGCGNGCG 800  
 QY 415 GCGGTGAGCGGAGCGGCGAGGCGTTCCTCAGAGAGCGCGCGCGCGCGCGCGCGCGCG 474  
 Db 799 CGCGGGGCG 740  
 QY 475 CGAGGACCGCGGTATAAGAAAGCCTCGTGGCGCTTGCCTCGGGCAGCGCGAGTTCCTCCCGCG 534  
 Db 739 CGGCNCCCGGGCG 580  
 QY 535 CCCCAGAGCCCCCG 562  
 Db 679 CCG 652

RESULT 8  
 CNS0091P/c  
 LOCUS  
 DEFINITION  
 Drosophila melanogaster genome survey sequence TET3 end of BAC #  
 BACH19D16 of RPCI-98 library from Drosophila melanogaster (fruit  
 fly), genomic survey sequence.  
 AL053013  
 AL053013.1 GI:4934461  
 GSS.  
 SOURCE  
 Drosophila melanogaster (fruit fly)  
 ORGANISM  
 Drosophila melanogaster  
 Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
 Ephydroidea; Drosophilidae; Drosophila.  
 1 (bases 1 to 925)  
 Genoscope.  
 Direct Submission  
 Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :  
 BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr  
 - Web : www.genoscope.cns.fr)  
 Determination of this BAC-end sequence was carried out as part of a  
 collaboration with the Berkeley Drosophila Genome Project (BDGP).  
 The BDGP is constructing a physical map of the Drosophila  
 melanogaster genome using these BACs. For further information  
 please see <http://www.fruitfly.org> The BDGP Drosophila  
 melanogaster BAC library was prepared by Kazutoyo Osogawa and  
 Aaron Mammose in Pieter de Jong's laboratory in the Department of  
 Cancer Genetics at the Roswell Park Cancer Institute in Buffalo,  
 NY. The library is named RPCI-98 and was constructed by partial  
 EcoRI digestion of Drosophila DNA provided by the BDGP from the  
 isogenic strain y2; cn bw sp, the same strain used for the BDGP's  
 p1 and EST libraries. A more detailed description of the library  
 and how to order individual BAC clones, the entire library, or  
 filters for hybridization from the BACPAC Resource Center can be

УВЕДОМЛЕНИЕ



BQ681076/c  
 LOCUS  
 DEFINITION  
 ACCESSION  
 VERSION  
 KEYWORDS  
 SOURCE  
 ORGANISM  
 REFERENCE  
 AUTHORS  
 TITLE  
 JOURNAL  
 COMMENT  
 BQ681076  
 AGENCOURT 8187867 NIH\_MGC\_112 Homo sapiens cdna clone IMAGE:6259803  
 5', mRNA sequence.  
 BQ681076  
 BQ681076.1 GI:21793755  
 EST.  
 Homo sapiens (human)  
 Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 NIH-MGC <http://mgc.nci.nih.gov/>.  
 National Institutes of Health, Mammalian Gene Collection (MGC)  
 Unpublished (1999)  
 Contact: Robert Strausberg, Ph.D.  
 Email: [cgapbs-f@mail.nih.gov](mailto:cgapbs-f@mail.nih.gov)  
 Tissue Procurement: DCTD/DTP  
 CDNA Library Preparation: Rubin Laboratory  
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
 DNA sequencing by: Agencourt Bioscience Corporation  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:  
<http://image.llnl.gov>  
 Plate: LLCW2417 row: 0 column: 04  
 High quality sequence stop: 315.  
 Location/Qualifiers  
 1..1065  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:6259803"  
 /tissue\_type="melanotic melanoma, cell line"  
 /lab\_host="DHI0B (phage-resistant)"  
 /clone\_lib="NIH MGC 112"  
 /note="Organ: skin; Vector: pOTB7; Site 1: XhoI; Site 2:  
 into EcoRI/XhoI sites using the following 5' adaptor:  
 GGCACGAG(G). Library constructed by Ling Hong in the  
 laboratory of Gerald M. Rubin (University of California,  
 Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and  
 Superscript II RT (Life Technologies). Note: this is a  
 NIH MGC Library."

Query Match 13.2%; Score 74.4; DB 13; Length 1065;  
Best Local Similarity 45.4%; Pred. No. 0.0048;  
Matches 255; Conservative 0; Mismatches 305; Indels 2; Gaps 1;

QY	2	GGCGGGGGAGCGCGCCGGGAGTGGAGGCTGATCTGCTTGGCTGGCTCCACCTCCGCCAGGC	61
Db	900	GGGGGGGGGGCGGGGGGGCGCGCGCGGGCGGGCGCGCGCGCGGCGCGGCGGCGGCGGCGCG	841
QY	62	GCGAAGAGCGCCCCACGAGGACCCCGAGTGCACCGTTCGGATCAGAGGC	121
Db	840	GGGGGGGGCGGGCGCGCCCGGCGGGGGGGCGGCGGCGCGCGCGCGCGCGCGCGCGCG	781
QY	122	AGGACCCAGGGAGCCAGGAACCTGCGCGCGCCCCCGCCCTGCGCTGGCGCGAGGGAAGTC	181
Db	780	GGGGCGCGGGGGCGGGGGCGGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGGGG	721
QY	182	CCTTCACGAGGGAAGTCTCCCTACCCGGCCAGACCTCTGAGGGGGGGCGGTGGGTCA	241
Db	720	GGGNGGGCGCGGGGCCCGCGCGGGCGCGGGGGCGCGGGGGCGCGCGCGCGGGGGCG	661
QY	242	GACCGCAACGCAAGTTCGGGGCGGGGTGGGCTCTCGCGGAGACAAGGCCGGGCTTGCC	301
Db	660	GGCGNGGGGGCGCGGGCGCGGGGGGGGGCGCGGGGGGGGGGCGCGCGCGGGGGGGGG	601
QY	302	TCTCTCAGAGGCCCCACGCGCTTCCAGAGGAAGTCTCTGAGGCGCCGGGCGAGGAGGG	361
Db	600	GCG--CCGGGGGGCGGCGCGGCGGNGCGGGGGGGCGGGCGGGCGGCGGGGGGGGGGGGG	543

QY	362	GGCACCGGCTTCCACAGGCCCCGCCGCAGCAGAAATTGGCCAGGGCACGCCGTGA	421
Dd	542	GGGGGGGGGGCCGG	483
QY	422	CGGAGCGGGCAGGGGCTTTCTCAGGAGCGGGCGAGGCGCGCTTGAGGGGCGAGGAC	481
Dd	482	CCGGCCCGGG	423
QY	482	CGGGTATAGAACCCVTCGTGGCTTCCTCCCGGGCAGCCGCAGGTTCCCGCGGCCCGAG	541
Dd	422	GGGGGGCCCCCGGG	363
QY	542	CCCCCGCGCCCGCGCGGAGG	563
Dd	362	GGCGGGCGGGGNNGGGGCGGG	341

RESULT 13  
 BG809572/c  
 LOCUS  
 DEFINITION  
 ACCESSION  
 VERSION  
 KEYWORDS  
 SOURCE  
 ORGANISM

```

BG809572      888 bp      mRNA      linear      EST 22-MAY-2001
mgct001xa14f Magnaporthe grisea Appressorium Stage cDNA Magnaporthe
grisea cDNA clone mgct001xa14f 5', mRNA sequence.

BG809572      GI:14180552
EST.
Magnaporthe grisea (anamorph: Pyricularia grisea)
Magnaporthe grisea
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Sordariomycetes Incertae sedis; Magnaporthaceae, Magnaporthe.
1 (bases 1 to 888)
Choi,W. and Dean,R.A.
Construction and sequence analysis of an appressorium stage cDNA
library in the rice blast fungus, Magnaporthe grisea
Unpublished (2001)
Contact: Ralph A. Dean
Fungal Genomics Laboratory
North Carolina State University
Campus Box 7251, Raleigh, NC 27695, USA
Tel: 919-513-0020
Fax: 919-513-0024
Email: ralph.dean@ncsu.edu
Seq primer: T3 primer (AATTAAACCCTCACTAAAGG).
Location/Qualifiers
1..888
/organism="Magnaporthe grisea"
/mol_type="mRNA"
/strain="w70-15"
/db_xref="taxon:148305"
/clone="mgct001xa14f"
/dev_stage="Germinated conidia on appressorium-inductive
surface"
/clone_lib="Magnaporthe grisea Appressorium Stage cDNA"
/note="Vector: pBlueScript SK(+); Vector; Site_1: EcoRI;
Site_2: XhoI; The appressorium formation-specific cDNA
library was constructed from conidia germinated for 5-8 hr
on an inductive surface. The library contains over 55,000
clones with average insert size of 1.5 kbp."
    
```

ORIGIN

Query Match 13.2%; Score 74.2; DB 12; Length 888;  
 Best Local Similarity 49.5%; Pred. No. 0.005;  
 Matches 213; Conservative 0; Mismatches 216; Indels 1; Gaps 1;

QY	132	GAGCAGGAACTCGCGCGCCCGCCCTGCGCGGAGGAGCTCCCTCACCNGA	191
Dd	820	GGCGCGCGCGCCCNCCC CGCGCCCGCGGNGGCGCGCGGGGGGGGGGGGGGGGGGG	761
QY	192	GGGAAGCTCCCTCACC CGGCCAGCCCTG CAGGGGGGGCGGTGGGGTCAGACCGCAAAG	251
Dd	760	GGGGCGCGGGGGGGGGGGGGCGCGCGCGCGCGCGGGGCGGGGCGCGGGGGGGGGGG	701
QY	252	CGAAGTGC GGCGCGGGGTGGCGCTCGCGGAGACAAGGCGCGGGCGCTGCTCTCTCAGAG	311

	ORIGIN	Clones with average insert size of 1.5 kbp.					
	Query Match	13.2%;	Score 74.2;	DB 12;	Length 888;		
	Best Local Similarity	49.5%;	Pred. No. 0.005;				
	Matches 213; Conservative	0;	Mismatches 216;	Indels 1;	Gaps 1;		
QY	132	GAGCCAGGAAC	TGCGCGCGGCCCGCCCTGCCTGGCGGAGGAAGTCCCTCACCNGA	191			
Db	820	GGCGCCGCGGCCN	CCCCCGCGCCCGCCGCGCGCGCGGGGGGGGGGGGGGG	761			
QY	192	GGGAAGCTCCCTCA	CCC CGCCG CCGAGCCCTG CAGGGGGGCGCGTG GGGGTG CAGACCCCAAAG	251			
Db	760	GGGGCGCGGGGGG	GGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG	701			
QY	252	CGAAGTGC GGCGCGGGGTGG	CGCTTCGCGGAGACA AAGCCCGGGCGCTGCTCTCTCAGAG	311			

Db 700 CGCGGGGGGCGCGCGGGCGGGCGCGCGCGCGGGCGGGCGCGCGCGCGCGCGCGCG 641  
 QY 312 GCGCCCGAGCGCCCTCCGAGAGGAGTCTCTCAGAGCGCGCGCGAGGAGGCGCACGGGCT 371  
 Db 640 GGGCGCGCGGGCGCGGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 581  
 QY 372 TCCAGAGGCG 430  
 Db 580 GCGCGCGCGCGCGCGGG 521  
 QY 431 GCAGGCGCTTCTCAGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 490  
 Db 520 CGGGCG 461  
 QY 491 GAAGCGCTTCTCAGAGCG 550  
 Db 460 CGGGCG 401  
 QY 551 CGGGCGCGGGG 560  
 Db 400 GCGGGGGCGG 391

RESULT 14  
 EG786331/c  
 LOCUS  
 DEFINITION  
 Strongylocentrotus purpuratus cDNA clone PC\_0028\_A2\_G12\_MR 5', mRNA sequence.  
 EG786331  
 EG786331.1 GI:14157344  
 EST.  
 SOURCE  
 Strongylocentrotus purpuratus  
 ORGANISM  
 Strongylocentrotus purpuratus  
 Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;  
 Echinioidea; Echinozoidea; Echinacea; Echinioidea;  
 Strongylocentrotidae; Strongylocentrotus.  
 REFERENCE  
 1 (bases 1 to 1040)  
 Zhu,X., Mahairas,G., Illies,M.R., Cameron,R.A., Davidson,E.H. and  
 Ettensohn,C.A.  
 A large scale analysis of mRNAs expressed by primary mesenchyme  
 cells of the sea urchin embryo  
 Development 128 (13), 2615-2627 (2001)  
 MEDLINE  
 21384984  
 PUBMED  
 11493577  
 CONTACT: Ettensohn CA  
 Dept. Biol. Sci.  
 Carnegie Mellon University  
 4400 Fifth Avenue, Pittsburgh, PA 15213, USA  
 Tel: +1 412 268 5849  
 Email: ettensohn@andrew.cmu.edu.  
 Location/Qualifiers  
 1. .1040  
 /organism="Strongylocentrotus purpuratus"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:7668"  
 /clone="PC\_0028\_A2\_G12\_MR"  
 /tissue\_type="embryo"  
 /cell\_type="primary mesenchyme cells"  
 /lab\_hosts="E.coli"  
 /clone\_lib="sea urchin primary mesenchyme cell cDNA  
 library"  
 /notes=Vector: pSPORT1; Site 1: NotI; Site 2: SalI; oligo  
 dt priming from poly A+ RNA, directionally cloned"

FEATURES  
 source  
 1. .1040  
 /organism="Strongylocentrotus purpuratus"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:7668"  
 /clone="PC\_0028\_A2\_G12\_MR"  
 /tissue\_type="embryo"  
 /cell\_type="primary mesenchyme cells"  
 /lab\_hosts="E.coli"  
 /clone\_lib="sea urchin primary mesenchyme cell cDNA  
 library"  
 /notes=Vector: pSPORT1; Site 1: NotI; Site 2: SalI; oligo  
 dt priming from poly A+ RNA, directionally cloned"

ORIGIN  
 Query Match 13.1%; Score 74; DB 12; Length 1040;  
 Best Local Similarity 46.9%; Pred. No. 0.0056;  
 Matches 261; Conservative 0; Mismatches 292; Indels 3; Gaps 1;  
 QY 7 GGGAGGCGCGCGGAGTGGCGCTGATCGCTCGGCGCTCCACCTCCCGAGCGCAGA 66  
 Db 872 GCG 813

QY 67 AGCGGCCACGAGGAGCCCGCAGTCCCGCAGTGTTCACCGTCTTGGGATCAGAGCGAGGGA 126  
 Db 812 GCGCGCGCGCGGGGGCGCGCGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 753  
 QY 127 CAGGAGCGCGAGAAATGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 186  
 Db 752 GGGCG 693  
 QY 187 CONAGAGGAAGTCCCTCACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 246  
 Db 692 GCG 633  
 QY 247 CAAAGCGAAGTTCG 306  
 Db 632 GCG 573  
 QY 307 CAGAGGCG 366  
 Db 572 CCG 513  
 QY 367 GGGCTTCCCGAGGCG 426  
 Db 512 GGGCG 453  
 QY 427 GCGGGCAGGCGCTTCTCAGGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 486  
 Db 452 GCG 394  
 QY 487 ATAAGAAAGCTTCGTGCGCTTTCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 546  
 Db 393 --CCG 336  
 QY 547 GCGCGCGCGCGCGCGGAG 562  
 Db 335 CCGCGCGCGCGCGCGCG 320

RESULT 15  
 AG043499/c  
 LOCUS  
 DEFINITION  
 Pan troglodytes DNA, clone: PTB-021N08.F, genomic survey sequence.  
 ACCESSION  
 AG043499  
 VERSION  
 AG043499.1 GI:16572224  
 KEYWORDS  
 GSS.  
 SOURCE  
 Pan troglodytes (chimpanzee)  
 ORGANISM  
 Pan troglodytes  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.  
 REFERENCE  
 1  
 Fujiyama,A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T.,  
 Totoki,Y., Watanabe,H. and Sakaki,Y.  
 BAC end sequences of Library PTB  
 AUTHORS  
 2 (bases 1 to 949)  
 Fujiyama,A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T.,  
 Totoki,Y., Watanabe,H. and Sakaki,Y.  
 Direct Submission  
 TITLE  
 Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical  
 and Chemical Research (RIKEN), Genomic Sciences Center (GSC);  
 1-7-22 Suehiro-chou,Tsukumi-ku, Yokohama, Kanagawa 230-0045, Japan  
 (E-mail:chimpes@sc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/  
 Tel:81-45-503-9111, Fax:81-45-503-9170)  
 Clones are derived from the chimpanzee BAC library PTB This BAC end  
 was generated during the R&D process and may have higher chance of  
 clone tracking errors.  
 PRIMERS  
 Sequencing: -21M13  
 LIBRARY  
 Vector : PKS145  
 R.Site 1 : SacI  
 R.Site 2 : SacI.  
 Location/Qualifiers

## COMMENT



source

1..949

/organism="Pan troglodytes"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:9598"  
/clone="PTB-021N08.F"  
/sex="male"  
/cell\_type="lymphoblast"  
/clone\_lib="PTB Chimpanzee Male BAC Library"

ORIGIN

Query Match 13.1%; Score 73.6; DB 29; Length 949;  
Best Local Similarity 44.9%; Fred. No. 0.0064;  
Matches 225; Conservative 0; Mismatches 267; Indels 9; Gaps 2;  
QY 57 CAGGCGCAGAGAGGCGCCGCCAGAGGACCCCACTGCCCCGACGTTGCCACGGTCTGGGATCA 116  
Db 849 CGGGCGGCGCGCGCCCGCGGCGCCCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 790  
QY 117 GAGGAGGAGCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 176  
Db 789 GGGCGGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 730  
QY 177 AGTCTCCTCACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 232  
Db 729 GCG 670  
QY 233 ---GTGGGGTCAAGCGCAAGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 289  
Db 669 GGGGGGGGCG 610  
QY 290 GCGGGGCTGCTCTCTCAGAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 349  
Db 609 GGNNGGCGGGGNGGNGGNGGNGGNGGNGGNGGNGGNGGNGGNGGNGGNGGNGGNGGNGGNG 550  
QY 350 GCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 409  
Db 549 GCGGNGGCGGGGCGCGCGGGGGGCGCGGGGGGCGCGGGGGGCGCGGGGGGCGCGGGGGGCG 492  
QY 410 GCACGGCGGTGAGCGGAGCGGGGAGGGGCTTTCTCAGGAGCGCGGCGGAGGCGCGGCGCTGG 469  
Db 491 GGGGGGCGGGGCGGGGCGGGGCGGGGCGGGGCGGGGCGGGGCGGGGCGGGGCGGGGCGGGG 432  
QY 470 AGGGCGGAGGACCGGGGTATAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 529  
Db 431 CGCGCGGGGCGGGGCGGGGCGGGGCGGGGCGGGGCGGGGCGGGGCGGGGCGGGGCGGGGCG 372  
QY 530 GCGCGCGCGGAGCG 550  
Db 371 GGGGCGGCGGGGCGGGGCGGGGCGGGGCGGGGCGGGGCGGGGCGGGGCGGGGCGGGGCGGG 351

Search completed: June 6, 2004, 18:42:05  
Job time : 2625 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 6, 2004, 15:41:42 ; Search time 406 Seconds  
(without alignments)  
5890.974 Million cell updates/sec

Title: SEQ19PLUS12

Perfect score: 563

Sequence: 1 cggccggaggagcgccggg.....ccgcgcgcgcggcgagg 563

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 3373863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : N\_Geneseq\_29Jan04.\*

1: Geneseqn1980s.\*

2: Geneseqn1990s.\*

3: Geneseqn2000s.\*

4: Geneseqn2001s.\*

5: Geneseqn2001bs.\*

6: Geneseqn2002s.\*

7: Geneseqn2003as.\*

8: Geneseqn2003bs.\*

9: Geneseqn2003cs.\*

10: Geneseqn2004s.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	298.4	53.0	1794	6	ABT06542 Human HRN
2	120	21.3	562	2	AAV54620 LU105 spe
3	117	20.8	190	2	AAV54616 LU105 spe
4	116	20.6	561	9	ADE39936 Human lun
5	92	16.3	543	3	AAZ29723 Human sig
6	92	16.3	543	3	AAZ298173 Human sig
7	78	13.9	519	2	AAV54621 LU105 pol
8	78	13.9	569	6	ABK40267 cDNA enco
9	78	13.9	570	3	AAZ65103 Membrane-
10	78	13.9	570	5	AAZ44249 Human PRO
11	78	13.9	570	7	ABX77974 Human PRO
12	78	13.9	570	7	ABX80386 Novel hum
13	78	13.9	570	7	ACA69292 Human cDN
14	78	13.9	570	7	ABX90363 Human sec
15	78	13.9	570	7	ABX64209 cDNA enco
16	78	13.9	570	7	ACA64431 Novel hum
17	78	13.9	570	7	ABX80890 Human sec
18	78	13.9	570	7	ACD44399 cDNA enco
19	78	13.9	570	7	ABX79570 Human sec
20	78	13.9	570	7	ACA93591 Novel hum
21	78	13.9	570	7	ABX81273 Novel hum
22	78	13.9	570	7	ACA93089 Novel hum
23	78	13.9	570	7	ABX17173 Human PRO

24	78	13.9	570	8	ACA68028	Novel hum
25	78	13.9	570	8	ACA88477	Human sec
26	78	13.9	570	8	ACD81984	cDNA enco
27	78	13.9	570	8	ADA37918	Human cDN
28	78	13.9	570	8	ADA21604	Human cDN
29	78	13.9	570	8	ADA10391	Human cDN
30	78	13.9	570	8	ADA17935	cDNA enco
31	78	13.9	570	8	ADA28043	Human cDN
32	78	13.9	570	8	ADA94623	Human cDN
33	78	13.9	570	8	ADA38848	Human cDN
34	78	13.9	570	8	ADA92969	Human cDN
35	78	13.9	570	8	ACH65545	Human cDN
36	78	13.9	570	8	ADA22530	Human cDN
37	78	13.9	570	8	ACD39535	Human cDN
38	78	13.9	570	8	ADA06696	Human sec
39	78	13.9	570	8	ADA39389	Human cDN
40	78	13.9	570	8	ADB96415	Human PRO
41	78	13.9	570	9	ADC57887	Human PRO
42	78	13.9	570	9	ADC55251	Human PRO
43	78	13.9	570	9	ADC12118	Human cDN
44	78	13.9	570	9	ADC56540	Human PRO
45	78	13.9	570	9	ADC07595	Human cDN

## ALIGNMENTS

### RESULT 1

ABT06542  
ID ABT06542 standard; DNA; 1794 BP.

XX  
AC ABT06542;

XX  
DT 07-NOV-2002 (first entry)

XX  
DE Human HIN-1 coding sequence.

XX  
KW Human; methylated gene; methylation; breast cancer; marker; WT-1;

XX  
KW cell proliferative disorder; TWIST; HOSAS; NES-1; FARbeta; cyclin D2;

XX  
KW retinoic acid receptor beta; oestrogen receptor; Wilms' tumour;

XX  
KW 14.3.3 sigma; HIN-1; RASSF1A; tumour suppressor gene; hypermethylation;

XX  
KW gene; promoter; ds.

XX  
OS Homo sapiens.

XX  
PN WO200259347-A2.

XX  
PD 01-AUG-2002.

XX  
PF 28-JAN-2002; 2002WO-US002455.

XX  
PR 26-JAN-2001; 2001US-00771357.

XX  
PA (UYJO ) UNIV JOHNS HOPKINS SCHOOL MEDICINE.

XX  
PI Sukumar S, Evron E, Dooley WC, Sacchi N, Davidson N, Fackler MJ;

XX  
PR WPI; 2002-599803/64.

XX  
DR Diagnosing and/or determining a predisposition to a cellular

XX  
PT proliferative disorder of breast tissue, in particular breast cancer, by

XX  
PT determining the state of methylation of one or more nucleic acids

XX  
XX isolated from the subject.

XX  
XX Disclosure; Fig 9A; 115pp; English.

XX  
XX The present invention relates to a method of diagnosing a cellular

XX  
XX proliferative disorder of breast tissue, which involves determining the

XX  
XX state of methylation of one or more nucleic acids isolated from the

XX  
XX subject, where the state of methylation of the nucleic acids as compared

XX  
XX with a state of methylation from a subject not having the cellular

XX  
XX proliferative disorder of breast tissue is indicative of a cellular

XX  
XX proliferative disorder of breast tissue in the subject. The nucleic acids



XX 31-JAN-1997; 97US-00791710.

XX (ABBO ) ABBOTT LAB.

XX Billing-Medel PA, Cohen M, Colpitts TL, Friedman PN, Gordon J;  
XX Granados EN, Hodges SC, Klass MR, Kratochvil JD, Robertsrap L;  
XX Russell JC, Stroupe SD;

XX WPI; 1998-437479/37.

XX New nucleic acid for the lung disease marker LUI05 - polypeptides,  
XX antibodies and genes, used for diagnosis, prevention, treatment of lung  
XX disease, specifically cancer.

XX Claim 11; Fig 1; 123pp; English.

XX Sequences shown in AAV54616 to AAV54621 represent LUI05 specific  
XX polynucleotide sequences. These are used in the method of the invention  
XX for detecting target LUI05 nucleic acid. The method comprises treating a  
XX sample with at least one LUI05 specific nucleic acid, or its complement  
XX which is at least 50 percent identical with the LUI05 specific nucleic  
XX acid sequences (AAV54616 to AAV54621). LUI05 is a lung disease marker.  
XX Cells transformed with a recombinant expression system that contains  
XX LUI05 specific nucleic acid fragments, are used to express recombinant  
XX LUI05 polypeptides which are used to raise antibodies. The antibodies are  
XX used to detect the LUI05 antigen, and correspondingly this antigen is  
XX used to detect specific antibodies, in usual immunoassays. The LUI05  
XX polypeptides and nucleic acid sequences are used for diagnosis, staging,  
XX monitoring, prognosis, prevention, treatment and determination of  
XX susceptibility to, lung disease, specifically cancer. The LUI05  
XX polypeptides are also used to screen for specific binding agents, useful  
XX therapeutically. LUI05 is a marker for lung disease (present at high  
XX concentration, in altered form or in an unusual body compartment). LUI05  
XX can be detected in blood, plasma or serum in an inexpensive, non-invasive  
XX test. (Updated on 25-MAR-2003 to correct PI field.)

XX Sequence 190 BP; 18 A; 69 C; 67 G; 32 T; 0 U; 4 Other;

XX Query Match 20.8%; Score 117; DB 2; Length 190;

XX Best Local Similarity 96.7%; Pred. No. 1.1e-13;  
XX Matches 117; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

XX 431 GCAGGGCTTTCTCAGGAGCGCGGCGAGCGCGCTGGAGGGCGAGGACCGGGTATAA 490  
XX 1 GCAGGGCTTTCTCAGGAGCGCGGCGAGCGCGCTGGAGGGCGAGGACCGGGTATAA 60

XX 491 GAAGCCTCGTGGCTTGGCCGGCGAGCGCGCAGGTTCCCGCGCGCCCGAGCCCGCGCG 550  
XX 61 GAGGCTCGTGGCTTGGCCGGCGAGCGCGCAGGTTCCCGCGCGCCCGAGCCCGCGCGC 120

XX 551 C 551

XX 121 C 121

XX RESULT 4

XX ADE39936  
XX ID ADE39936 standard; cDNA; 561 BP.

XX ADE39936;

XX 29-JAN-2004 (first entry)

XX Human lung disorder-related cDNA - SEQ ID 6.

XX pepsin C; lung disorder; human; ss.

XX Homo sapiens.

XX US2003124580-A1.

XX 03-JUL-2003.

XX 06-SEP-2002; 2002US-00237435.

XX 07-SEP-2001; 2001US-0317822P.

XX (INCY-) INCYTE GENOMICS INC.

XX Walker MG, Spiro PA, Murry LE;

XX WPI; 2003-810982/76.

XX New cDNAs co-expressed with lung surfactant and surfactant synthesis  
XX genes, useful as diagnostics in assessing the prognosis and treatment of  
XX a lung disorder, or as potential targets for identifying therapeutics for  
XX lung disorders.

XX Claim 2; SEQ ID NO 6; 29pp; English.

XX The invention relates to a novel isolated cDNA and a cDNA encoding pepsin  
XX C. The polynucleotide of the invention may be useful as a probe or a  
XX component within an expression vector, as a diagnostic in assessing the  
XX prognosis and treatment of a lung disorder and as a potential therapeutic  
XX or target for the identification of therapeutics for lung disorders.  
XX Furthermore, the polynucleotide may be used to produce purified proteins  
XX or peptides which can subsequently be used to produce antibodies. The  
XX current sequence is that of the human lung disorder-related cDNA (SEQ ID  
XX 6) of the invention.

XX Sequence 561 BP; 86 A; 200 C; 189 G; 86 T; 0 U; 0 Other;

XX Query Match 20.6%; Score 116; DB 9; Length 561;

XX Best Local Similarity 100.0%; Pred. No. 1.7e-13;

XX Matches 116; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX 436 GCTTTCTCAGGAGCGCGGCGAGCGCGCTGGAGGGCGAGGACCGGGTATAAGAGC 495  
XX 1 GCTTTCTCAGGAGCGCGGCGAGCGCGCTGGAGGGCGAGGACCGGGTATAAGAGC 60

XX 496 CTCGTGGCCTTGGCCGGCGAGCGCGCAGGTTCCCGCGCGCCCGAGCCCGCGGCC 551

XX 61 CTCGTGGCCTTGGCCGGCGAGCGCGCAGGTTCCCGCGCGCCCGAGCCCGCGGCC 116

XX RESULT 5

XX AAZ29723

XX ID AAZ29723 standard; DNA; 543 BP.

XX AAZ29723;

XX 27-MAR-2000 (first entry)

XX Human lung specific gene Lng107.

XX Lung Specific Gene; LSG; Lng107; human; diagnostic marker; prognosticate;  
XX lung cancer; diagnosis; ds.

XX Homo sapiens.

XX Key Location/Qualifiers

XX CDS 93..407

XX /\*tag= a

XX /product= "LSG Lng107 protein"

XX WO9960160-A1.

XX 25-NOV-1999.

XX 12-MAY-1999; 99WO-US010344.

XX 21-MAY-1998; 98US-0086212P.

XX (DIAD-) DIADEXUS LLC.

XX PA

PI Yang F, Macina RA, Sun Y;

XX WPI: 2000-116320/10.

DR P-PSDB; AAY44458.

XX

PT A new method for diagnosing, monitoring and staging lung cancer.

PS Claim 6; Page 36; 40pp; English.

XX

CC The present sequence is a lung specific gene (LSG) Lng107 from human  
 CC clone ID 586271. The LSG has high level of tissue specificity for lungs  
 CC and is overexpressed in cancerous tissues. The sequence serves as a  
 CC diagnostic marker for detecting, monitoring, staging and prognosticating  
 CC lung cancer. The diagnosis involves comparing levels of LSG in samples  
 CC obtained from patient and normal control

XX Sequence 543 BP; 89 A; 194 C; 178 G; 82 T; 0 U; 0 Other;

Query Match 16.3%; Score 92; DB 3; Length 543;

Best Local Similarity 100.0%; Pred. No. 6.7e-09;

Matches 92; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 460 CCGGCGCTGGAGGGGCGAGGACCGGGTATAGAGCCCTGCTGGCCCTGCCCGGGCAGCGG 519

Db 1 CCGGCGCTGGAGGGGCGAGGACCGGGTATAGAGCCCTGCTGGCCCTGCCCGGGCAGCGG 60

Qy 520 CAGGTTCCCGCGCGCGCCCGAGCCCGCGCC 551

Db 61 CAGGTTCCCGCGCGCGCCCGAGCCCGCGCC 92

XX

RESULT 6

AAZ98173

ID AAZ98173 standard; cDNA; 543 BP.

XX

AC AAZ98173;

XX

DT 11-MAY-2000 (first entry)

XX

DE Human signal peptide containing protein HSP-65 cDNA SEQ ID NO:199.

XX

KW Human; signal peptide-containing protein; HSP; diagnosis; cancer;  
 KW inflammation; cardiovascular disease; anticancer; anti-inflammatory;  
 KW antimicrobial; neurotropic; neuroprotective; cardiovascular; hepatotropic;  
 KW anasthmatic; gene therapy; cell proliferation; neurological disorder;  
 KW reproductive disorder; developmental disorder; arteriosclerosis;  
 KW cirrhosis; psoriasis; acquired immune deficiency syndrome; anaemia;  
 KW asthma; Crohn's disease; infection; Alzheimer's disease; schizophrenia;  
 KW Parkinson's disease; Huntington's diseases; ovulatory defect;  
 KW muscular dystrophy; ss.

XX

OS Homo sapiens.

XX

PN WO20000610-A2.

XX

PD 06-JAN-2000.

XX

PF 25-JUN-1999; 98WO-US014484.

XX

PR 26-JUN-1998; 98US-0090762P.

XX

PR 31-JUL-1998; 98US-0094983P.

XX

PR 01-OCT-1998; 98US-0102686P.

XX

PR 11-DEC-1998; 98US-0112129P.

XX

PA (INCY-) INCYTE PHARM INC.

XX

XX Lal P, Tang YT, Gorgone GA, Corley NC, Guegler KJ, Baughn MR;

PI Akerblom IE, Au-Young J, Yue H, Patterson C, Reddy R, Hillman JL;

PI Bandman O;

XX

XX WPI: 2000-160673/14.

DR P-PSDB; AAY87288.

PT New human signal peptide-containing proteins useful in treatment,  
 PT prevention and diagnosis of e.g. cancer, inflammation and cardiovascular  
 PT disease.

XX Claim 9; Page 289; 327pp; English.

XX

CC AAZ98109 to AAZ98242 encode AAY87224 to AAY87357 which represent the  
 CC human signal peptide-containing proteins HSP-1 to HSP-134. HSPPs have  
 CC anticancer, anti-inflammatory, antimicrobial, neurotropic, hepatotropic,  
 CC neuroprotective, cardiovascular and antiasthmatic activities, and can be  
 CC used in gene therapy. HSPPs can be used to treat or prevent disorders  
 CC associated with decreased activity or function of HSP. Antagonists of  
 CC HSP are used to treat or prevent disorders associated with increased  
 CC activity or function of HSP. Such diseases include cell proliferation  
 CC (including cancer), inflammation, cardiovascular, neurological,  
 CC reproductive or developmental disorders, (e.g. arteriosclerosis,  
 CC cirrhosis, psoriasis, acquired immune deficiency syndrome, anaemia,  
 CC asthma, Crohn's disease, microbial or other infections, congestive or  
 CC ischaemic heart disease, Alzheimer's, Parkinson's or Huntington's  
 CC diseases, schizophrenia, ovulatory defects, muscular dystrophy). HSPP  
 CC nucleic acids can be used for the recombinant production of HSP, for  
 CC detecting HSP in standard hybridisation and amplification assays (for  
 CC diagnosis and monitoring), in gene therapy, as antisense, triplex-forming  
 CC or ribozyme therapeutics, for detecting related sequences or genetic  
 CC variations, and for chromosomal mapping. HSPP are also used to raise  
 CC specific antibodies (Ab) and to screen for agonists and antagonists  
 CC (potential therapeutic agents). Ab are used to diagnose, or monitor, HSPP  
 CC -related diseases (in usual immunoassays), as therapeutic antagonists, in  
 CC competitive drug screens, and for purification of HSP from natural  
 CC sources

XX Sequence 543 BP; 89 A; 194 C; 178 G; 82 T; 0 U; 0 Other;

Query Match 16.3%; Score 92; DB 3; Length 543;

Best Local Similarity 100.0%; Pred. No. 6.7e-09;

Matches 92; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 460 CCGGCGCTGGAGGGGCGAGGACCGGGTATAGAGCCCTGCTGGCCCTGCCCGGGCAGCGG 519

Db 1 CCGGCGCTGGAGGGGCGAGGACCGGGTATAGAGCCCTGCTGGCCCTGCCCGGGCAGCGG 60

Qy 520 CAGGTTCCCGCGCGCCCGAGCCCGCGCC 551

Db 61 CAGGTTCCCGCGCGCCCGAGCCCGCGCC 92

XX

RESULT 7

AAV54621

ID AAV54621 standard; cDNA; 519 BP.

XX

AC AAV54621;

XX

DT 25-MAR-2003 (revised)

DT

DT 30-OCT-1998 (first entry)

XX

DE LU105 polypeptide encoding cDNA clone 1327836IH.

XX

KW LU105; lung disease marker; immunoassay; lung disease; cancer; blood;

KW plasma; serum; ss.

XX

OS Homo sapiens.

XX

PH Key Location/Qualifiers

FT CDS 79..393

FT /\*tag= a

FT /transl\_except= (pos:136..138, aa:Val)

FT /product= "LU105 polypeptide"

XX

PN WO9833926-A1.

XX

PD 06-AUG-1998.

XX

PF 30-JAN-1998; 98WO-US001766.

```
XX 31-JAN-1997; 97US-00791710.
XX (ABBO ) ABBOTT LAB.
XX
XX Billing-Medel PA, Cohen M, Colpitts TL, Friedman PN, Gordon J;
XX PI Granados EN, Hodges SC, Klass MR, Kratochvil JD, Robertsrap L;
XX PI Russell JC, Stroupe SD;
XX
XX WPI; 1998-437479/37.
XX DR P-PSDB; AAW5868.
XX
XX New nucleic acid for the lung disease marker LU105 - polypeptides,
XX antibodies and genes, used for diagnosis, prevention, treatment of lung
XX disease, specifically cancer.
XX
XX Claim 11; Fig 1; 123pp; English.
XX
XX Sequences shown in AAV54616 to AAV54621 represent LU105 specific
XX polynucleotide sequences. These are used in the method of the invention
XX for detecting target LU105 nucleic acid. The method comprises treating a
XX sample with at least one LU105 specific nucleic acid, or its complement
XX which is at least 50 percent identical with the LU105 specific nucleic
XX acid sequences (AAV54616 to AAV54621). LU105 is a lung disease marker.
XX Cells transformed with a recombinant expression system that contains
XX LU105 specific nucleic acid fragments, are used to express recombinant
XX LU105 polypeptides which are used to raise antibodies. The antibodies are
XX used to detect the LU105 antigen, and correspondingly this antigen is
XX used to detect specific antibodies, in usual immunoassays. The LU105
XX polypeptides and nucleic acid sequences are used for diagnosis, staging,
XX monitoring, prognosis, prevention, treatment and determination of
XX susceptibility to, lung disease, specifically cancer. The LU105
XX polypeptides are also used to screen for specific binding agents, useful
XX therapeutically. LU105 is a marker for lung disease (present at high
XX concentration, in altered form or in an unusual body compartment). LU105
XX can be detected in blood, plasma or serum in an inexpensive, non-invasive
XX test. (Updated on 25-MAR-2003 to correct PI field.)
XX
XX Sequence 519 BP; 78 A; 190 C; 170 G; 81 T; 0 U; 0 Other;
XX
XX Query Match 13.9%; Score 78; DB 2; Length 519;
XX Best Local Similarity 100.0%; Pred. No. 3.2e-06;
XX Matches 78; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 474 GCGAGGACCGGGTATAAGAGCCTCGTGGCTTCGCCGGGCGAGCCGCGAGTTCCTCCGCGC 533
XX 1 GCGAGGACCGGGTATAAGAGCCTCGTGGCTTCGCCGGGCGAGCCGCGAGTTCCTCCGCGC 60
XX
XX 534 GCCCGGAGCCCCCGCGCC 551
XX 61 GCCCGGAGCCCCCGCGCC 78
XX
XX RESULT 9
XX ABK40267
XX ID ABK40267 standard; cDNA; 569 BP.
XX
XX AC ABK40267;
XX
XX 15-JUL-2002 (first entry)
XX cDNA encoding human PRO1245 polypeptide.
XX
XX Human; PRO; benign tumour; malignant tumour; lymphoid malignancy;
XX leukaemia; neuronal disorder; stromal disorder; blastocoelec disorder;
XX inflammatory disorder; immune disorder; angiogenic disorder;
XX gene therapy; cytostatic; neuroprotective; gene; ss.
XX
XX Homo sapiens.
XX
XX WO200153486-A1.
XX
XX 26-JUL-2001.
```

```
XX 11-FEB-2000; 2000WO-US003565.
XX
XX 08-MAR-1999; 99WO-US005028.
XX 11-MAR-1999; 99US-0123972P.
XX 11-MAY-1999; 99US-0133459P.
XX 02-JUN-1999; 99WO-US012252.
XX 22-JUN-1999; 99US-0140650P.
XX 22-JUN-1999; 99US-0140653P.
XX 20-JUL-1999; 99US-0144758P.
XX 28-JUL-1999; 99US-0145698P.
XX 28-JUL-1999; 99US-0146222P.
XX 17-AUG-1999; 99US-0149395P.
XX 31-AUG-1999; 99US-0151689P.
XX 01-SEP-1999; 99WO-US020111.
XX 15-SEP-1999; 99WO-US021090.
XX 30-NOV-1999; 99WO-US028313.
XX 01-DEC-1999; 99WO-US028301.
XX 01-DEC-1999; 99WO-US028634.
XX 05-JAN-2000; 2000WO-US000219.
XX (GETH ) GENENTECH INC.
XX
XX Ashkenazi AU, Goddard A, Godowski PJ, Gurney AL, Hillan KJ;
XX PI Marsters SA, Pan J, Pitti RM, Roy MA, Smith V, Stone DM;
XX Watanabe CK, Wood WI;
XX WPI; 2002-205567/26.
XX P-PSDB; AAU86141.
XX
XX Thirty five nucleic acids encoding PRO polypeptides, useful for treating
XX benign or malignant tumors, leukemias and lymphoid malignancies,
XX inflammatory, angiogenic and immunologic disorders.
XX
XX Claim 50; Fig 27; 302pp; English.
XX
XX The present invention relates to the isolation of novel human PRO
XX polypeptides and the polynucleotide sequences encoding them. The PRO
XX polypeptides, agonists, antagonists or anti-PRO antibodies are useful for
XX treating benign or malignant tumors (e.g. renal, kidney, bladder,
XX breast, etc), leukaemias and lymphoid malignancies, other disorders such
XX as neuronal, glial, astrocytal, hypothalamic, glandular, macrophagal,
XX stromal and blastocoelec disorders, inflammatory, immune and angiogenic
XX disorders. The polynucleotide sequences are also useful in gene therapy.
XX ABK40254-ABK40288 encode for the human PRO polypeptides of the invention
XX
XX Sequence 569 BP; 128 A; 190 C; 170 G; 81 T; 0 U; 0 Other;
XX
XX Query Match 13.9%; Score 78; DB 6; Length 569;
XX Best Local Similarity 100.0%; Pred. No. 3.2e-06;
XX Matches 78; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 474 GCGAGGACCGGGTATAAGAGCCTCGTGGCTTCGCCGGGCGAGCCGCGAGTTCCTCCGCGC 533
XX 1 GCGAGGACCGGGTATAAGAGCCTCGTGGCTTCGCCGGGCGAGCCGCGAGTTCCTCCGCGC 60
XX
XX 534 GCCCGGAGCCCCCGCGCC 551
XX 61 GCCCGGAGCCCCCGCGCC 78
XX
XX RESULT 9
XX AAZ65103
XX ID AAZ65103 standard; cDNA; 570 BP.
XX
XX AC AAZ65103;
XX
XX 05-APR-2000 (first entry)
XX
XX Membrane-bound protein PRO1245 encoding cDNA.
XX
XX Membrane-bound polypeptide; PRO polypeptide; LDL receptor; TIE ligand;
XX pharmaceutical; receptor immunoadhesin; gene mapping; ss.
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```
XX OS Homo sapiens.
XX XX WO9963088-A2.
XX XX PD 09-DEC-1999.
XX XX PF 02-JUN-1999; 99WO-US012252.
XX PR 02-JUN-1998; 98US-0087607P.
XX PR 02-JUN-1998; 98US-0087609P.
XX PR 02-JUN-1998; 98US-0087759P.
XX PR 03-JUN-1998; 98US-0087827P.
XX PR 04-JUN-1998; 98US-0088021P.
XX PR 04-JUN-1998; 98US-0088025P.
XX PR 04-JUN-1998; 98US-0088028P.
XX PR 04-JUN-1998; 98US-0088029P.
XX PR 04-JUN-1998; 98US-0088030P.
XX PR 04-JUN-1998; 98US-0088033P.
XX PR 04-JUN-1998; 98US-0088036P.
XX PR 05-JUN-1998; 98US-0088167P.
XX PR 05-JUN-1998; 98US-0088202P.
XX PR 05-JUN-1998; 98US-0088212P.
XX PR 05-JUN-1998; 98US-0088217P.
XX PR 09-JUN-1998; 98US-0088655P.
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XX PR 10-JUN-1998; 98US-0088730P.
XX PR 10-JUN-1998; 98US-0088734P.
XX PR 10-JUN-1998; 98US-0088738P.
XX PR 10-JUN-1998; 98US-0088740P.
XX PR 10-JUN-1998; 98US-0088741P.
XX PR 10-JUN-1998; 98US-0088742P.
XX PR 10-JUN-1998; 98US-0088810P.
XX PR 10-JUN-1998; 98US-0088811P.
XX PR 10-JUN-1998; 98US-0088824P.
XX PR 10-JUN-1998; 98US-0088825P.
XX PR 10-JUN-1998; 98US-0088826P.
XX PR 11-JUN-1998; 98US-0088858P.
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XX PR 12-JUN-1998; 98US-0088876P.
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XX PR 16-JUN-1998; 98US-0089440P.
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XX PR 17-JUN-1998; 98US-0089600P.
XX PR 18-JUN-1998; 98US-0089653P.
XX PR 18-JUN-1998; 98US-0089801P.
XX PR 18-JUN-1998; 98US-0089907P.
XX PR 18-JUN-1998; 98US-0089908P.
XX PR 19-JUN-1998; 98US-0089947P.
XX PR 19-JUN-1998; 98US-0089948P.
XX PR 19-JUN-1998; 98US-0089952P.
XX PR 22-JUN-1998; 98US-0090246P.
XX PR 22-JUN-1998; 98US-0090252P.
XX PR 22-JUN-1998; 98US-0090254P.
XX PR 23-JUN-1998; 98US-0090349P.
XX PR 23-JUN-1998; 98US-0090355P.
XX PR 24-JUN-1998; 98US-0090429P.
XX PR 24-JUN-1998; 98US-0090431P.
XX PR 24-JUN-1998; 98US-0090435P.
XX PR 24-JUN-1998; 98US-0090444P.
XX PR 24-JUN-1998; 98US-0090445P.
XX PR 24-JUN-1998; 98US-0090461P.
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XX PR 24-JUN-1998; 98US-0090535P.
XX PR 24-JUN-1998; 98US-0090538P.
XX PR 24-JUN-1998; 98US-0090540P.
XX PR 24-JUN-1998; 98US-0090576P.
XX PR 25-JUN-1998; 98US-0090678P.
XX PR 25-JUN-1998; 98US-0090688P.
XX PR 25-JUN-1998; 98US-0090690P.
XX PR 25-JUN-1998; 98US-0090691P.
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XX PR 25-JUN-1998; 98US-0090695P.
XX PR 25-JUN-1998; 98US-0090696P.
XX PR 26-JUN-1998; 98US-0090862P.
XX PR 26-JUN-1998; 98US-0090863P.
XX PR 01-JUL-1998; 98US-0091358P.
XX PR 01-JUL-1998; 98US-0091360P.
XX PR 02-JUL-1998; 98US-0091478P.
XX PR 02-JUL-1998; 98US-0091486P.
XX PR 02-JUL-1998; 98US-0091519P.
XX PR 02-JUL-1998; 98US-0091544P.
XX PR 02-JUL-1998; 98US-0091626P.
XX PR 02-JUL-1998; 98US-0091628P.
XX PR 02-JUL-1998; 98US-0091633P.
XX PR 02-JUL-1998; 98US-0091646P.
XX PR 02-JUL-1998; 98US-0091673P.
XX PR 07-JUL-1998; 98US-0091978P.
XX PR 07-JUL-1998; 98US-0091982P.
XX PR 09-JUL-1998; 98US-0092472P.
XX PR 10-JUL-1998; 98US-0093339P.
XX PR 30-JUL-1998; 98US-0094651P.
XX PR 04-AUG-1998; 98US-0095282P.
XX PR 04-AUG-1998; 98US-0095285P.
XX PR 04-AUG-1998; 98US-0095301P.
XX PR 04-AUG-1998; 98US-0095302P.
XX PR 04-AUG-1998; 98US-0095318P.
XX PR 04-AUG-1998; 98US-0095321P.
XX PR 04-AUG-1998; 98US-0095325P.
XX PR 10-AUG-1998; 98US-0095916P.
XX PR 10-AUG-1998; 98US-0095929P.
XX PR 10-AUG-1998; 98US-0096012P.
XX PR 11-AUG-1998; 98US-0096143P.
XX PR 11-AUG-1998; 98US-0096146P.
XX PR 12-AUG-1998; 98US-0096529P.
XX PR 17-AUG-1998; 98US-0096757P.
XX PR 17-AUG-1998; 98US-0096766P.
XX PR 17-AUG-1998; 98US-0096768P.
XX PR 17-AUG-1998; 98US-0096773P.
XX PR 17-AUG-1998; 98US-0096791P.
XX PR 17-AUG-1998; 98US-0096867P.
XX PR 17-AUG-1998; 98US-0096891P.
XX PR 17-AUG-1998; 98US-0096894P.
XX PR 17-AUG-1998; 98US-0096895P.
XX PR 17-AUG-1998; 98US-0096897P.
XX PR 18-AUG-1998; 98US-0096949P.
XX PR 18-AUG-1998; 98US-0096950P.
XX PR 18-AUG-1998; 98US-0096959P.
XX PR 18-AUG-1998; 98US-0096960P.
XX PR 18-AUG-1998; 98US-0097022P.
XX PR 19-AUG-1998; 98US-0097141P.
XX PR 20-AUG-1998; 98US-0097218P.
XX PR 24-AUG-1998; 98US-0097661P.
XX PR 26-AUG-1998; 98US-0097951P.
XX PR 26-AUG-1998; 98US-0097952P.
XX PR 26-AUG-1998; 98US-0097954P.
XX PR 26-AUG-1998; 98US-0097955P.
XX PR 26-AUG-1998; 98US-0097971P.
XX PR 26-AUG-1998; 98US-0097974P.
XX PR 26-AUG-1998; 98US-0097978P.
XX PR 26-AUG-1998; 98US-0097979P.
XX PR 26-AUG-1998; 98US-0097986P.
XX PR 31-AUG-1998; 98US-0098014P.
XX PR 31-AUG-1998; 98US-0098525P.
XX PR 16-SEP-1998; 98US-0100634P.
XX PR 12-JAN-1999; 99US-0115565P.
XX XX
```

(GETH ) GENENTECH INC.

PA Baker K, Chen J, Goddard A, Gurney AL, Smith V, Watanabe CK;  
 XX Wood WI, Yuan J;  
 PI  
 PI  
 XX WPI; 2000-072883/06.  
 DR P-PSDB; AAY66757.

XX Membrane-bound proteins and related nucleotide sequences.

XX Claim 2; Fig 289; 822pp; English.

XX The invention provides membrane-bound PRO polypeptides and  
 CC polynucleotides encoding them. The PRO sequences of the invention were  
 CC identified based on extracellular domain homology screening. The PRO  
 CC sequences have homology with proteins including LDL receptors, TIE  
 CC ligands and various enzymes. The membrane-bound proteins and receptor  
 CC molecules are useful as pharmaceutical and diagnostic agents. Receptor  
 CC immunoadhesins, for instance, can be used as therapeutic agents to block  
 CC receptor-ligand interactions. The membrane-bound proteins can also be  
 CC employed for screening of potential peptide or small molecule inhibitors  
 CC of the relevant receptor/ligand interaction. The PRO encoding sequences  
 CC are useful as hybridization probes, in chromosome and gene mapping and in  
 CC the generation of antisense RNA and DNA. PRO nucleic acid sequences will  
 CC also be useful for the preparation of PRO polypeptides, especially by  
 CC recombinant techniques

XX Sequence 570 BP; 129 A; 190 C; 170 G; 81 T; 0 U; 0 Other;

Query Match 13.9%; Score 78; DB 3; Length 570;  
 Best Local Similarity 100.0%; Pred. No. 3.2e-06;

Matches 78; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 474 GCGAGGACCGGGTATAGAGCCTCGTGGCTTGCCTGGCGGCGAGCGGAGGTTCCCGCGC 533  
 DB 1 GCGAGGACCGGGTATAGAGCCTCGTGGCTTGCCTGGCGGCGAGCGGAGGTTCCCGCGC 60

QY 534 GCCCGGAGCCCCCGCGC 551

DB 61 GCCCGGAGCCCCCGCGC 78

RESULT 10

AAF44249

ID AAF44249 standard; cDNA; 570 BP.

XX AAF44249;

XX 02-APR-2001 (first entry)

XX Human PRO1245 (UNQ629) nucleotide sequence SEQ ID NO:407.

XX Human; secreted and transmembrane protein; PRO; cytostatic; cell death;  
 XX cancer; chromosomal mapping; gene mapping; tissue typing;  
 XX diagnostic assay; ss.

XX Homo sapiens.

XX WO200073454-A1.

XX 07-DEC-2000.

XX 30-MAR-2000; 2000WO-US008439.

XX 02-JUN-1999; 99WO-US012252.

XX 23-JUN-1999; 99US-0141037P.

XX 07-JUL-1999; 99US-0143048P.

XX 20-JUL-1999; 99US-0144758P.

XX 26-JUL-1999; 99US-0145698P.

XX 28-JUL-1999; 99US-0146222P.

XX 17-AUG-1999; 99US-0149396P.

XX 15-SEP-1999; 99WO-US021090.

XX 15-SEP-1999; 99WO-US021547.

PR 08-OCT-1999; 99US-0158663P.  
 PR 30-NOV-1999; 99WO-US028313.  
 PR 01-DEC-1999; 99WO-US028301.  
 PR 16-DEC-1999; 99WO-US030095.

PR 20-DEC-1999; 99WO-US030911.

PR 05-JAN-2000; 2000WO-US000219.

PR 06-JAN-2000; 2000WO-US000376.

PR 11-FEB-2000; 2000WO-US003565.

PR 18-FEB-2000; 2000WO-US004341.

PR 22-FEB-2000; 2000WO-US004414.

PR 24-FEB-2000; 2000WO-US004914.

PR 02-MAR-2000; 2000WO-US005004.

PR 15-MAR-2000; 2000WO-US006884.

PR 20-MAR-2000; 2000WO-US007377.

XX (GETH ) GENENTECH INC.

XX Ashkenazi AU, Baker KP, Botstein D, Desnoyers L, Eaton DL;

XX Ferrara N, Fong S, Gerber H, Gerritsen ME, Goddard A, Godowski PJ;

XX Grimaldi CJ, Gurney AL, Kijavini LJ, Napier MA, Pan J, Paoni NF;

XX Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM, Wood WI;

XX Zhang Z;

XX WPI; 2001-032160/04.

XX P-PSDB; AAB65280.

XX PRO polynucleotides used to produce polypeptides used to target bioactive

XX molecules such as toxins, radiolabels or antibodies, to specific cells,

XX to cause targeted cell death.

XX Claim 2; Fig 289; 935pp; English.

XX The present invention describes human secreted and transmembrane PRO

XX proteins. The PRO proteins have cytostatic activity. The PRO proteins can

XX be used for targeted delivery of bioactive molecules, such as toxins,

XX radiolabels or antibodies, that cause cell death. PRO nucleotide

XX sequences, and their fragments, can be used as hybridisation probes. in

XX chromosomal and gene mapping, and in the generation of anti-sense RNA and

XX DNA. They may also be used to produce transgenic animals which are used

XX to develop and screen therapeutically useful reagents. The PRO nucleotide

XX and protein sequence can be used for tissue typing and in treating

XX cancer. Anti-PRO antibodies can be used in diagnostic assays. AAF44270 to

XX AAF44470 represent PCR primers and hybridisation probes used in the

XX isolation of human PRO sequences. AAF44087 to AAF44269 and AAB65154 to

XX AAB65300 represent human PRO polynucleotide and protein sequences given

XX in the exemplification of the present invention

XX SQ Sequence 570 BP; 129 A; 190 C; 170 G; 81 T; 0 U; 0 Other;

XX Query Match 13.9%; Score 78; DB 5; Length 570;

XX Best Local Similarity 100.0%; Pred. No. 3.2e-06;

XX Matches 78; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 474 GCGAGGACCGGGTATAGAGCCTCGTGGCTTGCCTGGCGGCGAGCGGAGGTTCCCGCGC 533

DB 1 GCGAGGACCGGGTATAGAGCCTCGTGGCTTGCCTGGCGGCGAGCGGAGGTTCCCGCGC 60

QY 534 GCCCGGAGCCCCCGCGC 551

DB 61 GCCCGGAGCCCCCGCGC 78

RESULT 11

ABX77974

ID ABX77974 standard; cDNA; 570 BP.

XX ABX77974;

XX 14-APR-2003 (first entry)

XX Human PRO polynucleotide #127.



KW Human; PRO; gene; ss; cytostatic; tumour; cancer; breast; lung; stomach;  
KW liver; horse; cow; dog; cat; sheep; pig; goat; rabbit; ADEPT;  
KW antibody-dependent enzyme mediated prodrug therapy.

XX Homo sapiens.

XX US2003027163-A1.

XX 06-FEB-2003.

XX 15-NOV-2001; 2001US-00397666.

XX 16-JUN-1997; 97US-0049787P.

XX 17-OCT-1997; 97US-0062250P.

XX 05-NOV-1997; 97WO-US020069.

XX 12-NOV-1997; 97US-0065186P.

XX 13-NOV-1997; 97US-0065311P.

XX 24-NOV-1997; 97US-0066770P.

XX 25-FEB-1998; 98US-0075945P.

XX 20-MAR-1998; 98US-0078910P.

XX 28-APR-1998; 98US-0083322P.

XX 07-MAY-1998; 98US-0084600P.

XX 28-MAY-1998; 98US-0087106P.

XX 02-JUN-1998; 98US-0087607P.

XX 02-JUN-1998; 98US-0087609P.

XX 03-JUN-1998; 98US-0087759P.

XX 04-JUN-1998; 98US-0087827P.

XX 04-JUN-1998; 98US-0088021P.

XX 04-JUN-1998; 98US-0088025P.

XX 04-JUN-1998; 98US-0088026P.

XX 04-JUN-1998; 98US-0088028P.

XX 04-JUN-1998; 98US-0088029P.

XX 04-JUN-1998; 98US-0088030P.

XX 04-JUN-1998; 98US-0088032P.

XX 04-JUN-1998; 98US-0088326P.

XX 05-JUN-1998; 98US-0088167P.

XX 05-JUN-1998; 98US-0088202P.

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XX 10-JUN-1998; 98US-0088734P.

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XX 10-JUN-1998; 98US-0088810P.

XX 10-JUN-1998; 98US-0088824P.

XX 10-JUN-1998; 98US-0088826P.

PR 24-JUN-1998;

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PR 24-JUN-1998;

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PR 26-JUN-1998;

PR 26-JUN-1998;

PR 01-JUL-1998;

PR 01-JUL-1998;

PR 02-JUL-1998;

PR 02-JUL-1998;

PR 02-JUL-1998;

PR 02-JUL-1998;

PR 02-JUL-1998;

PR 07-JUL-1998;

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PR 20-JUL-1998;

PR 30-JUL-1998;

PR 04-AUG-1998;

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PR 11-AUG-1998;

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PR 12-AUG-1998;

PR 17-AUG-1998;

PR 17-AUG-1998;

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PR 17-AUG-1998;

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PR 18-AUG-1998;

98US-0090444P.

98US-0090445P.

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98US-0090535P.

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98US-0090542P.

98US-0090557P.

98US-0090676P.

98US-0090678P.

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98US-0090694P.

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98US-0090863P.

98US-0091360P.

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98US-0091626P.

98US-0091628P.

98US-0091833P.

98US-0091846P.

98US-0091673P.

98US-0091978P.

98US-0091982P.

98US-0092182P.

98US-0092472P.

98US-0093339P.

98US-0094651P.

98US-0095282P.

98US-0095301P.

98US-0095302P.

98US-0095318P.

98US-0095321P.

98US-0095325P.

98US-0095916P.

98US-0095929P.

98US-0096012P.

98US-0096143P.

98US-0096146P.

98US-0096329P.

98US-0096757P.

98US-0096766P.

98US-0096768P.

98US-0096773P.

98US-0096791P.

98US-0096867P.

98US-0096891P.

98US-0096894P.

98US-0096895P.

98US-0096897P.

98US-0096949P.

98US-0096950P.

98US-0096959P.

98US-0096960P.

98US-0097022P.

98US-0097141P.

98US-0097218P.

98US-0097661P.

98US-0097952P.

98US-0097954P.

98US-0097955P.

98US-0097971P.

98US-0097974P.

98US-0097978P.

98US-0097979P.

98US-0097986P.

98US-0098014P.

98US-0098525P.

98US-0100634P.

98WO-US019330.

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PR 17-SEP-1998; 98US-0100858P.
PR 17-SEP-1998; 98WO-US019437.
PR 17-OCT-1998; 98WO-US021141.
PR 01-DEC-1998; 98WO-US025108.
PR 22-DEC-1998; 98US-0113296P.
PR 05-JAN-1999; 98WO-US000106.
PR 08-MAR-1999; 98WO-US005028.
PR 12-MAR-1999; 98US-0123957P.
PR 02-JUN-1999; 98WO-US012252.
PR 23-JUN-1999; 98US-0141037P.
PR 07-JUL-1999; 98US-0143048P.
PR 20-JUL-1999; 98US-0144758P.
PR 26-JUL-1999; 98US-0145698P.
PR 28-JUL-1999; 98US-0146222P.
PR 17-AUG-1999; 98US-0149396P.
PR 15-SEP-1999; 98WO-US021090.
PR 08-OCT-1999; 98US-0158663P.
PR 30-NOV-1999; 98WO-US028313.
PR 01-DEC-1999; 98WO-US028301.
PR 01-DEC-1999; 98WO-US028634.
PR 16-DEC-1999; 98WO-US030095.
PR 20-DEC-1999; 98WO-US030911.
PR 05-JAN-2000; 2000WO-US000219.
PR 06-JAN-2000; 2000WO-US000376.
PR 11-FEB-2000; 2000WO-US003565.
PR 18-FEB-2000; 2000WO-US004341.
PR 22-FEB-2000; 2000WO-US004414.
PR 24-FEB-2000; 2000WO-US004914.
PR 24-FEB-2000; 2000WO-US005004.
PR 02-MAR-2000; 2000WO-US005841.
PR 10-MAR-2000; 2000WO-US006319.
PR 15-MAR-2000; 2000WO-US006884.
PR 20-MAR-2000; 2000WO-US007377.
PR 30-MAR-2000; 2000WO-US008439.
PR 15-MAY-2000; 2000WO-US013358.
PR 17-MAY-2000; 2000WO-US013705.
PR 22-MAY-2000; 2000WO-US014042.
PR 30-MAY-2000; 2000WO-US014941.
PR 02-JUN-2000; 2000WO-US015264.
PR 23-JUN-2000; 2000US-0213637P.
PR 28-JUL-2000; 2000WO-US020710.
PR 11-AUG-2000; 2000WO-US022031.
PR 23-AUG-2000; 2000WO-US023522.
PR 24-AUG-2000; 2000WO-US023328.
PR 07-SEP-2000; 2000US-0230978P.

Query Match 13.9%; Score 78; DB 7; Length 570;
Best Local Similarity 100.0%; Pred. No. 3.2e-06;
Matches 78; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 474 GCGAGGACCGGGTATAGAGAGCTCGTGGCTTGCCTGGCGGAGCGGAGGTTCCCGGCGC 533
Ddb 1 GCGAGGACCGGGTATAGAGAGCTTGCCTGGCGGAGCGGAGGTTCCCGGCGC 60

QY 534 GCCCGGAGCGCGCGGCGC 551
Ddb 61 GCCCGGAGCGCGCGGCGC 78

RESULT 12
ABX80386
ABX80386 standard; DNA; 570 BP.
ABX80386;
ABX80386;
28-APR-2003 (first entry)
Novel human secreted or transmembrane protein PRO1358 DNA.
Human; PRO; hypertrophy of neonatal heart; angiogenesis; wound healing;
cardiac insufficiency disorder; cancer; tumour; immune response;
adrenal cortical capillary endothelial growth; c-Fos induction;

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KW vascular endothelial growth factor inhibition; VEGF inhibition;
KW endothelial cell growth inhibitor; T-lymphocytes stimulation;
KW retinal neurons cell survival; rod photoreceptor cell survival;
KW retinal disorder; retinitis pigmentosa; kidney disorder;
KW mammalian kidney mesangial cell proliferation; Berger disease;
KW dermatitis; herpeticiformis; Crohn's disease; chondrocyte proliferation;
KW chondrocyte redifferentiation; sports injury; arthritis; genes; ds.
XX Homo sapiens.
OS US2002132252-A1.
PV 19-SEP-2002.
XX 14-NOV-2001; 2001US-00990442.
XX 16-JUN-1997; 97US-0049787P.
XX 17-OCT-1997; 97US-0062250P.
XX 05-NOV-1997; 97WO-US020069.
XX 12-NOV-1997; 97US-0065186P.
XX 13-NOV-1997; 97US-0065311P.
XX 24-NOV-1997; 97US-0066770P.
XX 25-FEB-1998; 98US-0075945P.
XX 20-MAR-1998; 98US-0078910P.
XX 28-APR-1998; 98US-0083322P.
XX 07-MAY-1998; 98US-0084600P.
XX 28-MAY-1998; 98US-0087106P.
XX 02-JUN-1998; 98US-0087607P.
XX 02-JUN-1998; 98US-0087609P.
XX 02-JUN-1998; 98US-0087759P.
XX 03-JUN-1998; 98US-0087827P.
XX 04-JUN-1998; 98US-0088021P.
XX 04-JUN-1998; 98US-0088036P.
XX 04-JUN-1998; 98US-0088028P.
XX 04-JUN-1998; 98US-0088029P.
XX 04-JUN-1998; 98US-0088030P.
XX 04-JUN-1998; 98US-0088033P.
XX 05-JUN-1998; 98US-0088167P.
XX 05-JUN-1998; 98US-0088202P.
XX 05-JUN-1998; 98US-0088212P.
XX 05-JUN-1998; 98US-0088217P.
XX 09-JUN-1998; 98US-0088655P.
XX 10-JUN-1998; 98US-0088734P.
XX 10-JUN-1998; 98US-0088738P.
XX 10-JUN-1998; 98US-0088742P.
XX 10-JUN-1998; 98US-0088810P.
XX 10-JUN-1998; 98US-0088824P.
XX 10-JUN-1998; 98US-0088826P.
XX 11-JUN-1998; 98US-0088858P.
XX 11-JUN-1998; 98US-0088861P.
XX 11-JUN-1998; 98US-0088876P.
XX 12-JUN-1998; 98US-0089105P.
XX 16-JUN-1998; 98US-0089440P.
XX 16-JUN-1998; 98US-0089512P.
XX 16-JUN-1998; 98US-0089514P.
XX 17-JUN-1998; 98US-0089532P.
XX 17-JUN-1998; 98US-0089538P.
XX 17-JUN-1998; 98US-0089598P.
XX 17-JUN-1998; 98US-0089599P.
XX 17-JUN-1998; 98US-0089600P.
XX 17-JUN-1998; 98US-0089653P.
XX 18-JUN-1998; 98US-0089801P.
XX 18-JUN-1998; 98US-0089907P.
XX 18-JUN-1998; 98US-0089908P.
XX 16-SEP-1998; 98WO-US019330.
XX 17-SEP-1998; 98WO-US019437.
XX 07-OCT-1998; 98WO-US021141.
XX 01-DEC-1998; 98WO-US025108.
XX 05-JAN-1999; 99WO-US000106.
XX 08-MAR-1999; 99WO-US005028.
XX 02-JUN-1999; 99WO-US012252.

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PR 15-SEP-1999; 99WO-US021090.  
 PR 15-SEP-1999; 99WO-US021547.  
 PR 30-NOV-1999; 99WO-US028131.  
 PR 01-DEC-1999; 99WO-US028301.  
 PR 01-DEC-1999; 99WO-US028634.  
 PR 16-DEC-1999; 99WO-US030095.  
 PR 20-DEC-1999; 99WO-US030911.  
 PR 06-JAN-2000; 2000WO-US000219.  
 PR 06-JAN-2000; 2000WO-US000376.  
 PR 11-FEB-2000; 2000WO-US003565.  
 PR 18-FEB-2000; 2000WO-US004341.  
 PR 22-FEB-2000; 2000WO-US004414.  
 PR 24-FEB-2000; 2000WO-US004914.  
 PR 24-FEB-2000; 2000WO-US005004.  
 PR 02-MAR-2000; 2000WO-US005841.  
 PR 10-MAR-2000; 2000WO-US006319.  
 PR 15-MAR-2000; 2000WO-US006884.  
 PR 20-MAR-2000; 2000WO-US007377.  
 PR 30-MAR-2000; 2000WO-US008439.  
 PR 15-MAY-2000; 2000WO-US013358.  
 PR 17-MAY-2000; 2000WO-US013705.  
 PR 22-MAY-2000; 2000WO-US014042.  
 PR 30-MAY-2000; 2000WO-US014941.  
 PR 02-JUN-2000; 2000WO-US015264.  
 PR 28-JUL-2000; 2000WO-US020710.  
 PR 11-AUG-2000; 2000WO-US022031.  
 PR 23-AUG-2000; 2000WO-US023522.  
 PR 24-AUG-2000; 2000WO-US023328.  
 PR 08-NOV-2000; 2000WO-US030952.  
 PR 01-DEC-2000; 2000WO-US032678.  
 PR 28-FEB-2001; 2001WO-US006520.  
 PR 01-JUN-2001; 2001WO-US017800.  
 PR 20-JUN-2001; 2001WO-US019692.  
 PR 29-JUN-2001; 2001WO-US021066.  
 PR 09-JUL-2001; 2001WO-US021735.  
 PR 28-AUG-2001; 2001US-00941992.

(GETH) GENENTECH INC.

XX ASHENAZI AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;  
 XX FERRARA N, Fong S, Gerber H, Gerritsen ME, Goddard A, Godowski P;  
 XX GRIMALDI JC, Gurney AL, Kljavin IG, Napier MA, Pan J, Paoni NP;  
 XX ROY MA, Stewart TA, Tumas D, Watanabe CK, Williams PM, Wood WT;  
 XX Zhang Z;

XX WPI; 2003-247083/24.  
 XX P-PSDB; AEU59174.

XX Novel isolated PRO polypeptides e.g., PRO826, PRO1068, PRO1184, PRO1346  
 XX and PRO1375, which stimulate proliferation of stimulated T-lymphocytes  
 XX are therapeutically useful for enhancing immune response and in cancer  
 XX treatments.

XX Claim 2; Fig 291; 648pp; English.

XX The invention describes an isolated human PRO polypeptide. The PRO  
 XX polypeptides are useful in detecting PRO polypeptides in a sample, in  
 XX linking a bioactive molecule to a cell expressing a PRO polypeptide, and  
 XX in modulating at least one biological activity of a cell expressing a PRO  
 XX polypeptide. PRO1312 stimulates hypertrophy of neonatal heart and is thus  
 XX useful for treating cardiac insufficiency disorders. PRO1154 and PRO1186  
 XX stimulate adrenal cortical capillary endothelial growth, and PRO536,  
 XX PRO943, PRO828, PRO826, PRO1068 or PRO535, PRO826, PRO819, PRO1126,  
 XX PRO1360 and PRO1387 induce c-fos in endothelial cells, and are thus  
 XX useful for treating conditions or disorders where angiogenesis would be  
 XX beneficial, e.g. wound healing and antagonism of this polypeptide are  
 XX useful for treating cancerous tumours. PRO812 inhibits vascular  
 XX endothelial growth factor (VEGF) stimulated proliferation of endothelial  
 XX cells and is thus useful for inhibiting endothelial cell growth in  
 XX mammals which would be beneficial in inhibiting tumour growth. PRO826,  
 XX PRO1068, PRO1184, PRO1346 and PRO1375 stimulate proliferation of  
 XX stimulated T-lymphocytes and are therapeutically useful for enhancing  
 XX immune response. PRO826, PRO1068 or PRO1132 enhance survival of

CC retinal neurons cells (PRO1132 is also enhances survival/proliferation of  
 CC rod photoreceptor cells) and therefore are useful for treating retinal  
 CC disorders of injuries, e.g. retinitis pigmentosa, AMD, PRO819, PRO813  
 CC and PRO1066 induce proliferation of mammalian kidney mesangial cells,  
 CC and therefore are useful for treating kidney disorders associated with  
 CC decreased mesangial cell function such as Berger disease or other  
 CC nephropathies associated with dermatitis, herpeticiformis or Crohn's  
 CC disease. PRO1310, PRO844, PRO1312, PRO1192 and PRO1387 induce the  
 CC proliferation and/or redifferentiation of chondrocytes in culture and are  
 CC thus useful for treating sports injuries, and arthritis. This sequence  
 CC represents a novel human PRO protein polynucleotide  
 XX

XX Sequence 570 BP; 129 A; 190 C; 170 G; 81 T; 0 U; 0 Other;

Query Match 13.9%; Score 78; DB 7; Length 570;  
 Best Local Similarity 100.0%; Pred. No. 3.2e-06;  
 Matches 78; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 474 GCGAGGACCGGGTATAGAGGCTCGTGCGCTTGCCCGGCGAGCGGTTCCCGCGC 533  
 |||  
 Db 1 GCGAGGACCGGGTATAGAGGCTCGTGCGCTTGCCCGGCGAGCGGTTCCCGCGC 60

QY 534 GCCCGAGCCCCCGGCC 551  
 |||  
 Db 61 GCCCGAGCCCCCGGCC 78

## RESULT 13

ACA69292  
 ID ACA69292 standard; cDNA; 570 BP.

XX ACA69292;

XX 26-JUN-2003 (first entry)

XX Human cDNA encoding secreted/transmembrane protein PRO1245.

XX Human; ss; gene; PRO; secreted protein; transmembrane protein;  
 XX cardiac insufficiency disorders; angiogenesis; wound healing;  
 XX cancerous tumour; immune response; retinal disorder; sight loss;  
 XX retinitis pigmentosa; age-related macular degeneration; AMD;  
 XX kidney disorder; Berger disease; nephropathy; dermatitis; herpeticiformis;  
 XX Crohn's disease; sports injury; arthritis.

XX Homo sapiens.

XX US2003032023-A1.

XX 13-FEB-2003.

XX 14-NOV-2001; 2001US-00990711.

XX 16-JUN-1997; 97US-0049787P.

XX 17-OCT-1997; 97US-0062250P.

XX 05-NOV-1997; 97WO-US020069.

XX 12-NOV-1997; 97US-0065186P.

XX 13-NOV-1997; 97US-0065311P.

XX 24-NOV-1997; 97US-0066770P.

XX 25-FEB-1998; 98US-0075945P.

XX 20-MAR-1998; 98US-0078910P.

XX 28-APR-1998; 98US-0083322P.

XX 07-MAY-1998; 98US-0084600P.

XX 28-MAY-1998; 98US-0087106P.

XX 02-JUN-1998; 98US-0087607P.

XX 02-JUN-1998; 98US-0087609P.

XX 02-JUN-1998; 98US-0087759P.

XX 03-JUN-1998; 98US-0087827P.

XX 04-JUN-1998; 98US-0088021P.

XX 04-JUN-1998; 98US-0088025P.

XX 04-JUN-1998; 98US-0088026P.

XX 04-JUN-1998; 98US-0088028P.

XX 04-JUN-1998; 98US-0088029P.

XX 04-JUN-1998; 98US-0088030P.



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PR 20-MAR-2000; 2000WO-US007377.
PR 30-MAR-2000; 2000WO-US008439.
PR 15-MAY-2000; 2000WO-US013358.
PR 17-MAY-2000; 2000WO-US013705.
PR 22-MAY-2000; 2000WO-US014042.
PR 30-MAY-2000; 2000WO-US014941.
PR 02-JUN-2000; 2000WO-US015264.
PR 23-JUN-2000; 2000US-0213637P.
PR 28-JUL-2000; 2000WO-US020710.
PR 11-AUG-2000; 2000WO-US022031.

Query Match      13.9%; Score 78; DB 7; Length 570;
Best Local Similarity 100.0%; Pred.No. 3.2e-06;
Matches 78; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 474 GCGAGGACCGGGTATAGAACCTTCGTCGCGGCGGAGCGGAGGTTCCCGCGC 533
Db 1 GCGAGGACCGGGTATAGAACCTTCGTCGCGGCGGAGCGGAGGTTCCCGCGC 60

QY 534 GCCCGGAGCCCCCGCGC 551
Db 61 GCCCGGAGCCCCCGCGC 78

RESULT 14
ABX90363
ID ABX90363 standard; cDNA; 570 BP.
AC ABX90363;
XX
XX DT (first entry)
XX 01-MAY-2003
XX Human secreted/transmembrane protein cDNA, #163.
DE
XX
XX Human; gene; ss; PRO; secreted; transmembrane; signal peptide;
KW pharmaceutical; diagnostic; therapeutic; gene therapy.
XX
XX Homo sapiens.
XX
XX US2002160384-A1.
XX
XX 31-OCT-2002.
XX
XX 14-NOV-2001; 2001US-00992598.
XX
XX 16-JUN-1997; 97US-0049787P.
XX 17-OCT-1997; 97US-0062250P.
XX 05-NOV-1997; 97WO-US020069.
XX 12-NOV-1997; 97US-0065186P.
XX 13-NOV-1997; 97US-0065311P.
XX 24-NOV-1997; 97US-0066770P.
XX 25-FEB-1998; 98US-0075945P.
XX 20-MAR-1998; 98US-0078910P.
XX 28-APR-1998; 98US-0083322P.
XX 07-MAY-1998; 98US-0084600P.
XX 28-MAY-1998; 98US-0087106P.
XX 02-JUN-1998; 98US-0087607P.
XX 02-JUN-1998; 98US-0087609P.
XX 02-JUN-1998; 98US-0087759P.
XX 03-JUN-1998; 98US-0087827P.
XX 04-JUN-1998; 98US-0088021P.
XX 04-JUN-1998; 98US-0088025P.
XX 04-JUN-1998; 98US-0088032P.
XX 04-JUN-1998; 98US-0088028P.
XX 04-JUN-1998; 98US-0088029P.
XX 04-JUN-1998; 98US-0088030P.
XX 04-JUN-1998; 98US-0088033P.
XX 04-JUN-1998; 98US-0088326P.
XX 05-JUN-1998; 98US-0088167P.
XX 05-JUN-1998; 98US-0088282P.
XX 05-JUN-1998; 98US-0088212P.
XX 05-JUN-1998; 98US-0088217P.
XX 09-JUN-1998; 98US-0088655P.
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PR 10-JUN-1998; 98US-0088734P.
PR 10-JUN-1998; 98US-0088738P.
PR 10-JUN-1998; 98US-0088742P.
PR 10-JUN-1998; 98US-0088810P.
PR 10-JUN-1998; 98US-0088824P.
PR 10-JUN-1998; 98US-0088826P.
PR 11-JUN-1998; 98US-0088858P.
PR 11-JUN-1998; 98US-0088861P.
PR 11-JUN-1998; 98US-0088876P.
PR 12-JUN-1998; 98US-0089105P.
PR 12-JUN-1998; 98US-0089440P.
PR 16-JUN-1998; 98US-0089512P.
PR 16-JUN-1998; 98US-0089514P.
PR 17-JUN-1998; 98US-0089532P.
PR 17-JUN-1998; 98US-0089538P.
PR 17-JUN-1998; 98US-0089598P.
PR 17-JUN-1998; 98US-0089599P.
PR 17-JUN-1998; 98US-0089600P.
PR 17-JUN-1998; 98US-0089653P.
PR 18-JUN-1998; 98US-0089801P.
PR 18-JUN-1998; 98US-0089907P.
PR 18-JUN-1998; 98US-0089908P.
PR 16-SEP-1998; 98WO-US019330.
PR 17-SEP-1998; 98WO-US019437.
PR 07-OCT-1998; 98WO-US021141.
PR 01-DEC-1998; 98WO-US025108.
PR 05-JAN-1999; 98WO-US000106.
PR 08-MAR-1999; 99WO-US005028.
PR 02-JUN-1999; 99WO-US012252.
PR 15-SEP-1999; 99WO-US021090.
PR 15-SEP-1999; 99WO-US021547.
PR 30-NOV-1999; 99WO-US028313.
PR 01-DEC-1999; 99WO-US028301.
PR 01-DEC-1999; 99WO-US028634.
PR 16-DEC-1999; 99WO-US030095.
PR 20-DEC-1999; 99WO-US030911.
PR 05-JAN-2000; 2000WO-US000219.
PR 06-JAN-2000; 2000WO-US000376.
PR 11-FEB-2000; 2000WO-US003565.
PR 18-FEB-2000; 2000WO-US004341.
PR 22-FEB-2000; 2000WO-US004414.
PR 24-FEB-2000; 2000WO-US004914.
PR 24-FEB-2000; 2000WO-US005004.
PR 02-MAR-2000; 2000WO-US005841.
PR 15-MAR-2000; 2000WO-US006319.
PR 20-MAR-2000; 2000WO-US006884.
PR 20-MAR-2000; 2000WO-US007377.
PR 30-MAR-2000; 2000WO-US008439.
PR 15-MAY-2000; 2000WO-US013358.
PR 17-MAY-2000; 2000WO-US013705.
PR 22-MAY-2000; 2000WO-US014042.
PR 30-MAY-2000; 2000WO-US014941.
PR 02-JUN-2000; 2000WO-US015264.
PR 28-JUL-2000; 2000WO-US020710.
PR 11-AUG-2000; 2000WO-US022031.
PR 23-AUG-2000; 2000WO-US023522.
PR 24-AUG-2000; 2000WO-US023328.
PR 08-NOV-2000; 2000WO-US030952.
PR 01-DEC-2000; 2000WO-US032678.
PR 28-FEB-2001; 2001WO-US006520.
PR 01-JUN-2001; 2001WO-US017800.
PR 20-JUN-2001; 2001WO-US019692.
PR 29-JUN-2001; 2001WO-US021066.
PR 03-JUL-2001; 2001WO-US021735.
PR 28-AUG-2001; 2001US-00941992.
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(GETH ) GENENTECH INC.

PI Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;  
PI Ferrara N, Fong S, Gerber H, Gerritsen ME, Goddard A, Godowski PJ;  
PI Grimaldi JC, Gurney AL, Kijavini IJ, Napier MA, Pan J, Paori NF;  
PI Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM, Wood WI;  
PI Zhang Z;

XX WPI; 2003-288106/28.  
DR P-PSDB; ABU60604.  
XX  
XX New transmembrane polypeptides and nucleic acids encoding the  
PT polypeptides, useful in gene therapy, in chromosome identification, as  
PT chromosome markers, or in generating probes.  
XX  
XX Claim 2; Fig 289; 650pp; English.  
XX  
XX The invention discloses isolated PRO secreted/transmembrane polypeptides  
XX comprising a sequence without signal peptide and the nucleic acid  
XX encoding them. The polypeptides can be used to raise antibodies that  
XX specifically bind to the PRO polypeptide, for linking a bioactive  
XX molecule to a cell expressing a PRO protein and for modulating at least  
XX one biological activity of a cell. The PRO polypeptides or  
XX polynucleotides are also useful in gene therapy, in chromosome  
XX identification, as chromosome markers, or in generating probes. The PRO  
XX polypeptides are useful as molecular markers for protein electrophoresis,  
XX and the isolated nucleic acids may be used for recombinantly expressing  
XX those markers. The PRO polypeptides and nucleic acids may also be used in  
XX tissue typing. Anti-PRO antibodies are useful in diagnostic assays for  
XX PRO, and in affinity purification of PRO from recombinant cell culture or  
XX natural sources. The sequences presented in ABX90083-ABX90468 are the  
XX genes encoding, the primers amplifying and the probes detecting the PRO  
XX polynucleotides of the invention. Note: The sequence data for this patent  
XX is also available in electronic format from USPTO at  
XX seqdata.uspto.gov/sequence.html  
XX  
XX Sequence 570 BP; 129 A; 190 C; 170 G; 81 T; 0 U; 0 Other;  
XX  
XX  
XX Query Match 13.9%; Score 78; DB 7; Length 570;  
XX Best Local Similarity 100.0%; Pred.No. 3.2e-06;  
XX Matches 78; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
XX  
Qy 474 GCGAGGACCGGTATAGACGCTTGCGCTTGCGGGGAGCGGAGGTTCGCCGGC 533  
Db 1 GCGAGGACCGGTATAGACGCTTGCGCTTGCGGGGAGCGGAGGTTCGCCGGC 60  
XX  
Qy 534 GCCCGAGCCCCCGGCC 551  
Db 61 GCCCGAGCCCCCGGCC 78  
XX  
RESULT 15  
ABX64209  
ID ABX64209 standard; cDNA; 570 BP.  
XX  
XX AC ABX64209;  
XX  
XX DT 26-FEB-2003 (first entry)  
XX  
XX DE cDNA encoding human PRO1245 polypeptide.  
XX  
XX KW Human; PRO polypeptide; secreted protein; transmembrane protein;  
KW genetic disorder; antibacterial; immunosuppressive; transgenic;  
KW gene therapy; gene; ss.  
XX  
XX OS Homo sapiens.  
XX  
XX PN US2002103125-A1.  
XX  
XX PD 01-AUG-2002.  
XX  
XX PF 20-NOV-2001; 2001US-00989731.  
XX  
XX PR 16-JUN-1997; 97US-0049787P.  
PR 17-OCT-1997; 97US-0062250P.  
PR 05-NOV-1997; 97WO-US020069.  
PR 12-NOV-1997; 97US-0065186P.  
PR 13-NOV-1997; 97US-0065311P.  
PR 24-NOV-1997; 97US-0066770P.  
PR 25-FEB-1998; 98US-0075945P.  
PR

20-MAR-1998; 98US-0078910P.  
28-APR-1998; 98US-0083322P.  
PR 07-MAY-1998; 98US-0084600P.  
PR 28-MAY-1998; 98US-0087106P.  
PR 02-JUN-1998; 98US-0087607P.  
PR 02-JUN-1998; 98US-0087609P.  
PR 02-JUN-1998; 98US-0087759P.  
PR 03-JUN-1998; 98US-0087827P.  
PR 04-JUN-1998; 98US-0088021P.  
PR 04-JUN-1998; 98US-0088025P.  
PR 04-JUN-1998; 98US-0088026P.  
PR 04-JUN-1998; 98US-0088028P.  
PR 04-JUN-1998; 98US-0088029P.  
PR 04-JUN-1998; 98US-0088030P.  
PR 04-JUN-1998; 98US-0088033P.  
PR 04-JUN-1998; 98US-0088326P.  
PR 05-JUN-1998; 98US-0088167P.  
PR 05-JUN-1998; 98US-0088202P.  
PR 05-JUN-1998; 98US-0088212P.  
PR 05-JUN-1998; 98US-0088217P.  
PR 09-JUN-1998; 98US-0088655P.  
PR 10-JUN-1998; 98US-0088734P.  
PR 10-JUN-1998; 98US-0088738P.  
PR 10-JUN-1998; 98US-0088742P.  
PR 10-JUN-1998; 98US-0088810P.  
PR 10-JUN-1998; 98US-0088824P.  
PR 10-JUN-1998; 98US-0088826P.  
PR 11-JUN-1998; 98US-0088858P.  
PR 11-JUN-1998; 98US-0088861P.  
PR 11-JUN-1998; 98US-0088876P.  
PR 12-JUN-1998; 98US-00889105P.  
PR 16-JUN-1998; 98US-0089440P.  
PR 16-JUN-1998; 98US-0089512P.  
PR 16-JUN-1998; 98US-0089514P.  
PR 17-JUN-1998; 98US-0089532P.  
PR 17-JUN-1998; 98US-0089538P.  
PR 17-JUN-1998; 98US-0089598P.  
PR 17-JUN-1998; 98US-0089599P.  
PR 17-JUN-1998; 98US-0089600P.  
PR 17-JUN-1998; 98US-0089653P.  
PR 18-JUN-1998; 98US-0089801P.  
PR 18-JUN-1998; 98US-0089907P.  
PR 18-JUN-1998; 98US-0089908P.  
PR 16-SEP-1998; 98WO-US019330.  
PR 17-SEP-1998; 98WO-US019437.  
PR 07-OCT-1998; 98WO-US021141.  
PR 01-DEC-1998; 98WO-US025108.  
PR 05-JAN-1999; 99WO-US000106.  
PR 08-MAR-1999; 99WO-US005028.  
PR 02-JUN-1999; 99WO-US012252.  
PR 15-SEP-1999; 99WO-US021090.  
PR 15-SEP-1999; 99WO-US021547.  
PR 30-NOV-1999; 99WO-US028313.  
PR 01-DEC-1999; 99WO-US028301.  
PR 01-DEC-1999; 99WO-US028634.  
PR 16-DEC-1999; 99WO-US030095.  
PR 20-DEC-1999; 99WO-US030911.  
PR 06-JAN-2000; 2000WO-US000219.  
PR 06-JAN-2000; 2000WO-US000376.  
PR 11-FEB-2000; 2000WO-US003565.  
PR 18-FEB-2000; 2000WO-US004341.  
PR 22-FEB-2000; 2000WO-US004414.  
PR 24-FEB-2000; 2000WO-US004914.  
PR 24-FEB-2000; 2000WO-US005004.  
PR 02-MAR-2000; 2000WO-US005841.  
PR 10-MAR-2000; 2000WO-US006319.  
PR 15-MAR-2000; 2000WO-US006884.  
PR 30-MAR-2000; 2000WO-US007377.  
PR 15-MAY-2000; 2000WO-US008439.  
PR 15-MAY-2000; 2000WO-US013358.  
PR 22-MAY-2000; 2000WO-US013705.  
PR 30-MAY-2000; 2000WO-US014042.  
PR 30-MAY-2000; 2000WO-US014941.



GenCore version 5.1.6  
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DM nucleic - nucleic search, using sw model

Run on: June 6, 2004, 15:43:12 ; Search time 3796 Seconds  
(without alignments)  
6428.379 Million cell updates/sec

Title: SEQ19PLUS12

Perfect score: 563

Sequence: 1 cggccgggagcgccggg.....cccgccggcggggagg 563

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : GenEmbl.\*

1: gb ba.\*

2: gb htg.\*

3: gb in.\*

4: gb om.\*

5: gb ov.\*

6: gb pat.\*

7: gb ph.\*

8: gb pl.\*

9: gb pr.\*

10: gb ro.\*

11: gb sts.\*

12: gb sy.\*

13: gb un.\*

14: gb vi.\*

15: em ba.\*

16: em fun.\*

17: em hum.\*

18: em in.\*

19: em mu.\*

20: em om.\*

21: em or.\*

22: em ov.\*

23: em pat.\*

24: em ph.\*

25: em pl.\*

26: em ro.\*

27: em sts.\*

28: em un.\*

29: em vi.\*

30: em htg hum.\*

31: em htg inv.\*

32: em htg other.\*

33: em htg mus.\*

34: em htg pln.\*

35: em htg rod.\*

36: em htg mam.\*

37: em htg vrt.\*

38: em sy.\*

39: em htgo hum.\*

40: em htgo mus.\*

41: em htgo other.\*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
C 1	488.6	86.8	127488	2	AC022095	AC022095 Homo sapi
C 2	486	86.3	168347	2	AC025336	AC025336 Homo sapi
C 3	486	86.3	190024	9	AC122714	AC122714 Homo sapi
C 4	478.8	85.0	130129	2	AC108083	AC108083 Homo sapi
5	475	84.4	166777	2	AC106813	AC106813 Homo sapi
6	120	21.3	562	6	BD082141	BD082141 Reagents
7	117	20.8	190	6	BD082137	BD082137 Reagents
8	92	16.3	543	6	BD222719	BD222719 Human sig
9	92	16.3	543	6	BD226775	BD226775 A novel m
10	78	13.9	519	6	BD082142	BD082142 Reagents
11	78	13.9	569	6	AX201348	AX201348 Sequence
12	78	13.9	570	6	AR252648	AR252648 Sequence
13	78	13.9	570	6	AX403520	AX403520 Sequence
14	78	13.9	570	9	AX359064	AX359064 Homo sapi
15	77	13.7	244	6	BD082138	BD082138 Reagents
C 16	74.4	13.2	172650	2	AF005772	AF005772 Oryza sat
C 17	74	13.1	125020	9	AF429315	AF429315 Homo sapi
C 18	70	12.4	1279	11	PM2H12G	AL684840 Penicilli
19	69	12.3	138709	2	BX649540	BX649540 Danio rer
20	68	12.1	167624	2	AC143286	AC143286 Macaca mu
C 21	68	12.1	219952	2	AC084804	AC084804 Mus muscu
22	67.4	12.0	63082	2	AC022663	AC022663 Homo sapi
23	67.2	11.9	183305	2	BX640474	BX640474 Danio rer
24	67	11.9	991	11	PM12H12B	AL684455 Penicilli
C 25	64.8	11.5	63082	2	AC022663	AC022663 Homo sapi
C 26	64.6	11.5	1094	11	PM7G11B	AL685196 Penicilli
C 27	64.2	11.4	240957	9	AC011407	AC011407 Homo sapi
28	63.8	11.3	1052	11	PM2H12B	AL684839 Penicilli
29	63.6	11.3	101509	2	AC027353	AC027353 Homo sapi
C 30	63.2	11.2	1007	11	PM3H11G	AL685749 Penicilli
C 31	63	11.2	65351	2	AC139773	AC139773 Homo sapi
32	62.8	11.2	956	11	PM2D12B	AL684743 Penicilli
33	62.4	11.1	125020	9	AF429315	AF429315 Homo sapi
C 34	62.2	11.0	129506	2	AC136100	AC136100 Rattus no
35	62.2	11.0	181850	2	BX276102	BX276102 Danio rer
C 36	62.2	11.0	224777	2	AC138109	AC138109 Mus muscu
37	62	11.0	154890	2	BX548249	BX548249 Danio rer
C 38	61.8	11.0	976	11	PM12D6G	AL684370 Penicilli
C 39	61.8	11.0	72645	2	AC112672	AC112672 Mus muscu
C 40	61.8	11.0	187413	2	AC141871	AC141871 Mus muscu
41	61.6	10.9	1965	10	AF411253	AF411253 Mus muscu
C 42	61.6	10.9	167077	2	AC091093	AC091093 Papio anu
C 43	61.4	10.9	239130	2	AC079420	AC079420 Mus muscu
C 44	60.8	10.8	885	11	PM7F8G	AL685189 Penicilli
45	60.6	10.8	1065	11	PM2B12B	AL684695 Penicilli

## ALIGNMENTS

RESULT 1  
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LOCUS AC022095 127488 bp DNA linear HTG 20-APR-2001  
DEFINITION Homo sapiens chromosome 5 clone CTB-36B8, WORKING DRAFT SEQUENCE,  
13 unordered pieces.  
ACCESSION AC022095  
VERSION AC022095.5 GI:13699618  
KEYWORDS HTG; HTGS PHASE1; HTGS\_DRAFT; HTGS\_ACTIVEFIN.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 127488)  
AUTHORS DOE Joint Genome Institute.  
TITLE Sequencing of Human Chromosome 5



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JOURNAL Unpublished
REFERENCE 2 (bases 1 to 127488)
AUTHORS DOE Joint Genome Institute.
TITLE Direct Submission
JOURNAL Submitted (26-JAN-2000) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
COMMENT On Apr 20, 2001 this sequence version replaced gi:7711676.
-----Genome Center
Center: Joint Genome Institute
Center Code: JGI
Web site: http://www.jgi.doe.gov
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Project Information
Center Project Name: 78060
Center clone name: CIT978SKB_36B8
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Summary Statistics
Consensus quality: 110477 bases at least Q40
Consensus quality: 117221 bases at least Q30
Consensus quality: 120225 bases at least Q20
Estimated insert size: 131000; pulse field gel estimation
Estimated insert size: 126288; sum-of-contigs estimation
Quality coverage: 7.48 in Q20 bases; pulse field gel estimation
Quality coverage: 7.76 in Q20 bases; sum-of-contigs estimation.
* NOTE: This is a 'working draft' sequence. It currently
* consists of 13 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
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* 1 1116: contig of 1116 bp in length
* 1117 1216: gap of unknown length
* 1217 2254: contig of 1038 bp in length
* 2255 2355: gap of unknown length
* 2355 3412: contig of 1058 bp in length
* 3413 3512: gap of unknown length
* 3513 5005: contig of 1493 bp in length
* 5006 5105: gap of unknown length
* 5106 7647: contig of 2542 bp in length
* 7648 7748: gap of unknown length
* 7748 10237: contig of 2490 bp in length
* 10238 10338: gap of unknown length
* 10338 12441: contig of 2103 bp in length
* 12441 12541: gap of unknown length
* 12541 15935: contig of 3395 bp in length
* 15936 16035: gap of unknown length
* 16036 24397: contig of 8361 bp in length
* 24397 24497: gap of unknown length
* 24497 39085: contig of 14599 bp in length
* 39086 39185: gap of unknown length
* 39186 60545: contig of 21360 bp in length
* 60546 60646: gap of unknown length
* 60646 79491: contig of 18845 bp in length
* 79491 79591: gap of unknown length
* 79591 127488: contig of 47838 bp in length.
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* Location/Qualifiers
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* /mol type="genomic DNA"
* /db xref="taxon:9606"
* /chromosome="5"
* /clone="CIB-36B8"
* /clone_lib="CalTech human BAC library B"
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Best Local Similarity 95.88; Pred. No. 3.1e-72;
Matches 529; Conservative 0; Mismatches 5; Indels 18; Gaps 2;
QY 1 CGGCGGAGGCGGCGGAGTGGAGCTGTGCTGGCGCTCCACCTCCCGAGG 60
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Db 84291 CGGCGGAGGCGGCGGAGTGGAGCTGTGCTGGCGCTCCACCTCCCGAGG 84232
QY 61 CGCAGAAAGGCGCCACAGAGGACCCCGAGTGGCCAGCTTGCACAGTCTGGGATCAGAGG 120
Db 84231 CGCAGAAAGGCGCCACAGAGGACCCCGAGTGGCCAGCTTGCACAGTCTGGGATCAGAGG 84172
QY 121 CAGGGACACAGGAGGCGCAGGAACTGGCGCGCCCGCCCGCTCCCTTGGCGCGAGGAAAGCT 180
Db 84171 CAGGACACAGGAGGCGCAGGAACTGGCGCGCCCGCCCGCTCCCTTGGCGCGAGGAAAGCT 84112
QY 181 CCCTACACNAGAGGAAAGCTTCCCTTCAACCGCGCCAGACCCCTCGAGGGGGCGCGTGGGTC 240
Db 84111 CCCCCCTCAC-----CCGGGCCACAGCCCTCGAGGGGGCGCGTGGGTC 84069
QY 241 AGACCGCAAGCGAGAGTGGCGCGCGGGTGGGCTCGCGGAGACAAAGGCCGCGCTGC 300
Db 84068 AGACCGCAAGCGAGAGTGGCGCGCGGGTGGGCTCGCGGAGACAAAGGCCGCGCTGC 84009
QY 301 CT-CTCTCAGAGGGCGCCCGCAGCGCTTCTCAGAGAGGAAAGTCTCTGAGGGCGCGGAGGAAAG 359
Db 84008 CTGCTCTCAGAGGGCGCCCGCAGCGCTTCTCAGAGAGGAAAGTCTCTGAGGGCGCGGAGGAAAG 83949
QY 360 GGGGACAGGGGCTTCCAGGGCGCGCGCGCGCGCAGAGGAAAGTGGCCAGGCGAGCGCCGT 419
Db 83948 GGGGACAGGGGCTTCCAGGGCGCGCGCGCGCGCAGAGGAAAGTGGCCAGGCGAGCGCCGT 83889
QY 420 GAGCGGAGCGGCGAGGGCTTCTCAGGAGCGCGGCGAGCGCGCGCTGAGGGCGCGAGG 479
Db 83888 GAGCGGAGCGGCGAGGGCTTCTCAGGAGCGCGGCGAGCGCGCGCTGAGGGCGCGAGG 83829
QY 480 ACCGGGTATAAGAGCTCTGCGGCTTCCCGGGCAGCGCGAGGTTCCCGCGCGCGCGCG 539
Db 83828 ACCGGGTATAAGAGCTCTGCGGCTTCCCGGGCAGCGCGAGGTTCCCGCGCGCGCGCG 83769
QY 540 AGCCCCCGCGCC 551
Db 83768 AGCCCCCGCGCC 83757

RESULT 2
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LOCUS Homo sapiens chromosome 5 clone RP11-451H23 map 5, WORKING DRAFT
DEFINITION SEQUENCE, 32 unordered pieces.
ACCESSION AC025336
VERSION AC025336.2 GI:7328761
KEYWORDS HTG; HTGS_PHASE1; HTGS_DRAFT.
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 168347)
AUTHORS Birren,B., Linton,L., Nusbaum,C. and Lander,B.
TITLE Homo sapiens chromosome 5, clone RP11-451H23
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 168347)
AUTHORS Birren,B., Linton,L., Nusbaum,C., Lander,B., Bastien,V., Beda,F.,
Anderson,S., Baldwin,J., Barna,N., Brown,A., Burkett,G.,
Boguslavsky,L., Boukhgalter,B., Brown,A., Colangelo,M., Collins,S.,
Campomano,A., Cooke,P., Dearellano,K., Dewar,K., Diaz,J.S.,
Collipere,A., Cooke,P., Choepel,Y., Colangelo,M., Collins,S.,
Dodge,S., Domino,M., Doyle,M., Ferreira,P., FitzHugh,W., Gage,D.,
Galagan,J., Gardyna,S., Ginde,S., Goyette,M., Graham,L.,
Grand-Pierre,N., Grant,G., Hagos,B., Heaford,A., Horton,L.,
Howland,J.C., Iliev,I., Johnson,R., Jones,C., Kann,L., Karatas,A.,
Klein,J., LaRocque,K., Lamazares,R., Landers,T., Lechoczy,J.,
Levine,R., Lieu,C., Liu,G., Locke,K., Macdonald,P., Marquis,N.,
McCarthy,M., McEwan,P., McGurk,A., McKernan,K., McPheeters,R.,
Meldrum,J., Meneus,L., Miranda,C., Mlenga,V., Morrow,J.,
Murphy,T., Naylor,J., Norman,C.H., O'Connor,T., O'Donnell,P.,
O'Neill,D., Olivier,T.M., Oliver,J., Peterson,K., Pierre,N.,
Pisani,C., Pollara,V., Raymond,C., Riley,R., Rogov,P., Rothman,D.,
Roy,A., Santos,R., Schauer,S., Severy,P., Spencer,B.,

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[illegible]

RESULT 3	
AC122714/c	
LOCUS	AC122714
DEFINITION	Homo sapiens chromosome 5 clone RP11-451H23, complete sequence.
ACCESSION	AC122714
	190024 bp DNA linear PRI 04-MAR-2003

AC122714.2	GI:28827858
HTG.	
KEYWORDS	
SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE	1 (bases 1 to 190024)
AUTHORS	DOE Joint Genome Institute and Stanford Human Genome Center.
TITLE	Direct Submission
REFERENCE	2 (bases 1 to 190024)
AUTHORS	DOE Joint Genome Institute.
TITLE	Direct Submission
JOURNAL	Submitted (25-MAY-2002) Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
REFERENCE	3 (bases 1 to 190024)
AUTHORS	DOE Joint Genome Institute and Stanford Human Genome Center.
TITLE	Direct Submission
JOURNAL	Submitted (04-MAR-2003) DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
COMMENT	On Mar 4, 2003 this sequence version replaced gi:21206277. Draft Sequence Produced by DOE Joint Genome Institute www.jgi.doe.gov Finishing Completed at Stanford Human Genome Center www.shgc.stanford.edu Quality: Phrap Quality >40 99.8% of Sequence; Estimated Total Number of Errors is 0.9 NOTE: Shatter libraries failed to verify the dinucleotide repeat region 124370-125308. Unsure number of repeat copies 124370-125308. Forced join 124996. Location/Qualifiers 1. .190024 /organism="Homo sapiens" /mol_type="genomic DNA" /db_xref="taxon:9606" /chromosome="5" /clone="RP11-451H23" 124370. .125308 misc_feature /note="NOTE: Shatter libraries failed to verify the dinucleotide repeat region 124370-125308. Unsure number of repeat copies 124370-125308. Forced join 124996."
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misc_feature	
origin	
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Matches	528; Conservative 0; Mismatches 5; Indels 19; Gaps 2;
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QY	61 CGCAGAAGCGCCACGAGAGCCCGACGTGCCCGACGCTTGCACACGCTCTGGGATCAGAGG 120
Db	81411 CGCAGAAGCGCCACGAGAGCCCGACGTGCCCGACGCTTGCACACGCTCTGGGATCAGAGG 81352
QY	121 CAGGACACAGGAGCGAGAACTGGCGCGCCCCCGCCCTCGCTGGCGCGAGGGAAGCT 180
Db	81351 CAGGACACAGGAGCGAGAACTGGCGCGCCCCCGCCCTCGCTGGCGCGAGGGAAGCT 81292
QY	181 CCCTCACCGNAGGGAAGCTCCCTCTCACCCGGGCCACAGCCCTCGAGGGGGCGCGTGGGGTC 240
Db	81291 C-----CCCTCACCGGCCACAGCCCTCGAGGGGGCGCGTGGGGTC 81250
QY	241 AGACCCGAAGCGAAGGTGCGGGCGGGGTGGGCTCGCGGAGACAAGAGCCGGGCGCTGC 300
Db	81249 AGACCCGAAGCGAAGGTGCGGGCGGGGTGGGCTCGCGGAGACAAGAGCCGGGCGCTGC 81190
QY	301 CT-CTTCAGAGGGCCCGAGCGCTTGCACAAGAGGAAGTCCTCGAGGCCCGGCGAGGAG 359
Db	81189 CTGCTCTCAGAGGGCCCGAGCGCTTGCACAAGAGGAAGTCCTCGAGGCCCGGCGAGGAG 81130
QY	360 GGGGCGACGGGCTTCCAGAGGGCCCGCGCGCAGCAGGAAGTTGGCCAGGGCACGGCGCT 419

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81129 GGGCAACGGCTTCCCGAGGGCCCGCGCAGCAGGAAAGTTGGCCAGGCAACGGCGGT 81070
420 CAGCGGAGCGGCGAGGCTTTCTCAGGAGCGCGGCGAGGCGCGCGCTGAGGCGCGAGG 479
81069 GAGCGGAGCGGCGAGGCTTTCTCAGGAGCGCGGCGAGGCGCGCGCTGAGGCGCGAGG 81010
480 ACCGGGTATAGAAAGCTCGTGGCTTCCCGGCGCAGCGCAGGTTCCCGCGGCGCGCG 539
81009 ACCGGGTATAGAAAGCTCGTGGCTTCCCGGCGCAGCGCAGGTTCCCGCGGCGCGCG 80950
540 AGCCCCCGCGC 551
80949 AGCCCCCGCGC 80938
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RESULT 4
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LOCUS
DEFINITION Homo sapiens chromosome 5 clone CTD-2013L15, WORKING DRAFT
SEQUENCE, 4 unordered pieces.
AC108083
ACCESSION AC108083.1 GI:18369929
VERSION HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_ACTIVEFIN.
KEYWORDS Homo sapiens (human)
SOURCE
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 130129)
DOE Joint Genome Institute.
Sequencing of Human Chromosome 5
Unpublished
2 (bases 1 to 130129)
DOE Joint Genome Institute.
Direct Submission
Submitted (25-JAN-2002) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
-----Genome Center
Center: Joint Genome Institute
Center Code: JGI
Web site: http://www.jgi.doe.gov
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Project Information
Center Project Name: 632820
Center clone name: CITB-H1_2013L15
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Summary Statistics
Consensus quality: 124488 bases at least Q40
Consensus quality: 128031 bases at least Q30
Consensus quality: 128842 bases at least Q20
Estimated insert size: 135000; agarose-fp estimation
Quality coverage: 7.66 in Q20 bases; agarose-fp estimation
Quality coverage: 7.97 in Q20 bases; sum-of-contigs estimation.
* NOTE: This is a 'working draft' sequence. It currently
* consists of 4 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
1 4320: contig of 4320 bp in length
* 4321 4420: gap of unknown length
* 4421 23712: contig of 12922 bp in length
* 23712 23812: gap of unknown length
* 23813 48602: contig of 24790 bp in length
* 48603 48702: gap of unknown length
* 48703 130129: contig of 81427 bp in length.
Location/Qualifiers
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/chromosome="5"
/clone="CTD-2013L15"
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ORIGIN
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Best Local Similarity 95.3%; Pred. No. 1.3e-70;
Matches 522; Conservative 0; Mismatches 7; Indels 19; Gaps 2;

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Db 24569 CGCGCGGAGGCGCGCGGAGTGAAGCTTATCTCTGGCGCTTCCACCTTCCACCTCCCGAGG 24510
Qy 61 CGCAGAAAGCGCGCCACGAGGACCCCGAGTGCCTCCGACGTTGTCACGCTCTGGATCAAGG 120
Db 24509 CGCAGAAAGCGCGCCACGAGGACCCCGAGTGCCTCCGACGTTGTCACGCTCTGGATCAAGG 24450
Qy 121 CAGGACACGAGGACCGAGGAAGTCTGCGCGCGCGCGCGCGCTTCCCTTGGCGGAGGAAGCT 180
Db 24449 CAGGACACGAGGACCGAGGAAGTCTGCGCGCGCGCGCGCGCTTCCCTTGGCGGAGGAAGCT 24390
Qy 181 CCCTCACGNGAGGGAAGCTTCCCTTCCACCGCGCGCGCGCGCGCTTCCCTTGGCGGAGGAAGCT 240
Db 24389 C-----CCCTTCCACCGCGCGCGCGCGCGCTTCCCTTGGCGGAGGAAGCT 24348
Qy 241 AGACCGCAAGCGAAGTGTGGCGCGCGCGCGCGCGCTTCCCTTGGCGGAGGAAGCTTCCCTTGGCGGAGGAAGCT 300
Db 24347 AGACCGCAAGCGAAGTGTGGCGCGCGCGCGCGCGCTTCCCTTGGCGGAGGAAGCTTCCCTTGGCGGAGGAAGCT 24288
Qy 301 CT-CTCTCAGAGGCGCGCGCGCGCGCGCTTCCCTTGGCGGAGGAAGCTTCCCTTGGCGGAGGAAGCT 359
Db 24287 CTGCTCTCAGAGGCGCGCGCGCGCGCGCTTCCCTTGGCGGAGGAAGCTTCCCTTGGCGGAGGAAGCT 24228
Qy 360 GGGGACAGGCGCTTCCACGAGGCGCGCGCGCGCGCGCTTCCCTTGGCGGAGGAAGCTTCCCTTGGCGGAGGAAGCT 419
Db 24227 GGGGACAGGCGCTTCCACGAGGCGCGCGCGCGCGCGCTTCCCTTGGCGGAGGAAGCTTCCCTTGGCGGAGGAAGCT 24168
Qy 420 GAGCGGAGCGGCGCGCGCGCGCGCGCTTCTCAGAGGCGCGCGCGCGCGCGCTTCTCAGAGGCGCGCGCGCGCGCG 479
Db 24167 GAGCGGAGCGGCGCGCGCGCGCGCGCTTCTCAGAGGCGCGCGCGCGCGCGCTTCTCAGAGGCGCGCGCGCGCGCG 24108
Qy 480 ACCGGGTATAGAAAGCTCGTGGCTTCCCGGCGCAGCGCGCGCGCGCGCGCTTCCCGCGCGCGCGCGCG 539
Db 24107 ACCGGGTATAGAAAGCTCGTGGCTTCCCGGCGCAGCGCGCGCGCGCGCGCTTCCCGCGCGCGCGCGCG 24048
Qy 540 AGCCCCCGC 547
Db 24047 AGCCCCCGC 24040

RESULT 5
AC106813
LOCUS
DEFINITION Homo sapiens chromosome 5 clone RP11-586L9, WORKING DRAFT SEQUENCE,
3 ordered pieces.
AC106813
ACCESSION AC106813.3 GI:19224876
VERSION HTG; HTGS_PHASE2; HTGS_DRAFT; HTGS_ACTIVEFIN.
KEYWORDS Homo sapiens (human)
SOURCE
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 16677)
DOE Joint Genome Institute.
AUTHORS
TITLE Sequencing of Human Chromosome 5
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 16677)
AUTHORS DOE Joint Genome Institute.
TITLE Direct Submission
JOURNAL Submitted (12-JAN-2002) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
REFERENCE 3 (bases 1 to 16677)
AUTHORS DOE Joint Genome Institute.
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RESULT 7
BD082137
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
Medel,P.A.B., Cohen,M., Colpitts,T.L., Friedman,P.N., Gordon,J.,
Granados,E.N., Hodges,S.C., Klass,M.R., Kratochvil,J.D., Rapp,L.R.,
Russell,J.C. and Stroupe,S.D.
Reagents and methods useful for detecting diseases of the lung
Patent: JP 2001522225-A 1 13-NOV-2001;
ABBOTT LABORATORIES
PN JP 2001522225-A/1
PD 13-NOV-2001
PF 30-JAN-1998 JP 1998533078
PR 31-JAN-1997 US 08/791710
PI PATRICIA A BILLING MEDEL, MAURICE COHEN, TRACEY L COLPITTS, PAULA
N FRIEDMAN,
PI JULIAN GORDON, EDWARD N GRANADOS, STEVEN C HODGES, MICHAEL R PI
KLASS,
PI JON D KRATOCHVIL, LISA ROBERTS RAPP, JOHN C RUSSELL, STEPHEN D
PI STROUPE
PC C12N15/63, C12N5/10, C12Q1/68, C07K14/47//C07K16/30, G01N33/574 CC
Strandedness: Single;
CC Topology: Linear;
FH Key Location/Qualifiers.
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Matches 117; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
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Ddb 1 GCAGGCGCTTCTCAGGNGCGCGGGCGAGCGCGCGTGGAGGGCGAGGACCGGGTATAA 60
QY 491 GAAGCCTCGTGCCCTTGCCTGGCGGCGAGCGCGAGTTCCCGCGCGCGCCCGAGCCCGCGGC 550
Ddb 61 GAGCGCTCGTGCCCTTGCCTGGCGGCGAGCGCGAGTTCCCGCGCGCGCCCGAGCCCGCGGC 120
QY 551 C 551
Ddb 121 C 121
RESULT 8
BD222719
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Human signal peptide-containing protein.
BD222719
BD222719.1 GI:33032489
JP 2002519030-A/65.
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Lal,P., Tang,Y.T., Gorgone,G.A., Corley,N.C., Guegler,K.J.,
REFERENCE
1 (bases 1 to 543)
AUTHORS

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Baughn,M.R., Akerblom,I.E., Young,J.A., Yue,H., Patterson,C.,
Reddy,R., Hillman,J.L. and Bandman,O.
Human signal peptide-containing protein
Patent: JP 2002519030-A 65 02-JUL-2002;
INCYTE PHARMACEUTICALS INC
OS Homo sapiens (human)
PN JP 2002519030-A/65
PD 02-JUL-2002
PF 25-JUN-1999 JP 2000557363
PR 26-JUN-1998 US 60/090762 31-JUL-1998 US 60/094983 PR
01-OCT-1998 US 60/102686 11-DEC-1998 US 60/112129 PI PREETI
LAL,Y TOM TANG,GINA A GORGONE,NEIL C CORLEY,KARL J PI GUEGLER,
PI MARIAH R BAUGHN,INGRID E AKERBLOM,JANICE AU YOUNG,HENRY YUE,
PI CHANDRA PATTERSON,ROOPA REDDY,JENNIFER L HILLMAN,OLGA BANDMAN
PC C12N15/09,A61K38/00,A61K39/395,A61K45/00,A61P9/00,A61P15/00,
PC A61P25/00,
PC A61P29/00,A61P35/00,A61P43/00,C07K14/47,C07K16/18,C12N1/15, PC
C12N1/19,
PC C12N1/21,C12N5/10,C12P21/02,C12Q1/68,G01N33/68//C12P21/08, PC
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PC A61K37/02,C12N5/00
CC Incyte Clone No: 3120415
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Best Local Similarity 100.0%; Pred. No. 7.8e-06;
Matches 92; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 460 CCGCGCTGGAGGGCGAGGACCGGGTATAGAGCCTCGTGGCTTCCCGGCGAGCGG 519
Ddb 1 CCGCGCTGGAGGGCGAGGACCGGGTATAGAGCCTCGTGGCTTCCCGGCGAGCGG 60
QY 520 CAGGTTCCCGCGCGCGCGCGAGCCCGCGCC 551
Ddb 61 CAGGTTCCCGCGCGCGCGCGAGCCCGCGCC 92
RESULT 9
BD226775
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
A novel method of diagnosing, monitoring and staging lung cancer.
BD226775
BD226775.1 GI:33036545
JP 2002515262-A/6.
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Yang,F., Macina,R.A. and Sun,Y.
A novel method of diagnosing, monitoring and staging lung cancer
Patent: JP 2002515262-A 6 28-MAY-2002;
DIADEXUS INC
OS Homo sapiens (human)
PN JP 2002515262-A/6
PD 28-MAY-2002
PF 12-MAY-1999 JP 2000549766
PR 21-MAY-1998 US 60/086212
PI FEI YANG,ROBERTO A MACINA,YONGMING SUN
PC C12N15/09,C12Q1/68,G01N33/50,C12N15/00
CC A novel method of diagnosing, monitoring and staging lung CC
cancer
FH Key Location/Qualifiers
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Best Local Similarity 100.0%; Pred. No. 7.8e-06;
Matches 92; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 520 CAGTTTCCCGCGCGCGCCCGGAGCCCGCGCGCC 551
Db 61 CAGTTTCCCGCGCGCGCCCGGAGCCCGCGCGCC 92
RESULT 10
LOCUS BD082142 519 bp DNA linear PAT 27-AUG-2002
DEFINITION Reagents and methods useful for detecting diseases of the lung.
ACCESSION BD082142
VERSION BD082142.1 GI:22627752
KEYWORDS JP 2001522225-A/6.
SOURCE Zea mays
ORGANISM Zea mays
REFERENCE
  AUTHORS Medel,P.A.B., Cohen,M., Colpitts,T.L., Friedman,P.N., Gordon,J.,
    Granados,E.N., Hodges,S.C., Klass,M.R., Kratochvil,J.D., Rapp,L.R.,
    Russell,J.C. and Stroupe,S.D.
  TITLE Reagents and methods useful for detecting diseases of the lung
  JOURNAL Patent: JP 2001522225-A 6 13-NOV-2001;
  COMMENT ABBOTT LABORATORIES
    PN JP 2001522225-A/6
    PD 13-NOV-2001
    PF 30-JAN-1998 JP 1998533078
    PR 31-JAN-1997 US 08/791710
    PI PATRICIA A BILLING MEDEL, MAURICE COHEN, TRACEY L COLPITTS, PAULA
      N FRIEDMAN,
      PI JULIAN GORDON, EDWARD N GRANADOS, STEVEN C HODGES, MICHAEL R PI
        KLASS,
        PI JON D KRATOCHVIL, LISA ROBERTS RAPP, JOHN C RUSSELL, STEPHEN D
          PI STROUPE
          PC C12N15/63, C12N5/10, C12Q1/68, C07K14/47//C07K16/30, G01N33/574 CC
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            CC Topology: Linear;
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Best Local Similarity 100.0%; Pred. No. 0.0016;
Matches 78; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 1 GCGAGGACCGGGTATAAGAGCCTCGTGGCTTGGCCGGCGGCGGCGGCGGCGGCGG 60
QY 534 GCCCGGAGCCCGCGCGCC 551
Db 61 GCCCGGAGCCCGCGCGCC 78

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RESULT 11
LOCUS AX201348 569 bp DNA linear PAT 30-AUG-2001
DEFINITION Sequence 27 from Patent WO0153486.
ACCESSION AX201348
VERSION AX201348.1 GI:15391167
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE
  AUTHORS Ashkenazi,A.J., Goddard,A., Godowski,P.J., Gurney,A.L.,
    Hillan,K.J., Marsters,S.A., Pan,J., Pitti,R.M., Roy,M.A., Smith,V.,
    Stone,D.M., Watanabe,C.K. and Wood,W.I.
  TITLE Compositions and methods for the treatment of tumour
  JOURNAL Patent: WO 0153486-A 27 26-JUL-2001;
  FEATURES Location/Qualifiers
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Best Local Similarity 100.0%; Pred. No. 0.0016;
Matches 78; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 1 GCGAGGACCGGGTATAAGAGCCTCGTGGCTTGGCCGGCGGCGGCGGCGGCGGCGG 60
QY 534 GCCCGGAGCCCGCGCGCC 551
Db 61 GCCCGGAGCCCGCGCGCC 78
RESULT 12
LOCUS AR252648 570 bp DNA linear PAT 20-DEC-2002
DEFINITION Sequence 407 from patent US 6478825.
ACCESSION AR252648
VERSION AR252648.1 GI:27300556
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 570)
AUTHORS Winterbottom,J.M., Shimp,L., Boyce,T.M. and Kaes,D.
TITLE Implant, method of making same and use of the implant for the
  treatment of bone defects
  JOURNAL Patent: US 6478825-A 407 12-NOV-2002;
  FEATURES Location/Qualifiers
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QY 534 GCCCGGAGCCCGCGCGCC 551
Db 61 GCCCGGAGCCCGCGCGCC 78

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RESULT 13
LOCUS      AX403520
DEFINITION Sequence 407 from Patent WO0073454.
ACCESSION  AX403520
VERSION     AX403520.1 GI:21437002
KEYWORDS   Homo sapiens (human)
SOURCE      Homo sapiens (human)
ORGANISM    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
AUTHORS     Askenazi A.J., Baker K.P., Botstein D., Desnovers L., Eaton D.,
            Ferrara N., Gerber H., Gritsenko M., Goddard A., Godowski P.,
            Grimaldi C.J., Gurney A.L., Kijavits I., Napier M.A., Pan J.,
            Paoni N.F., Roy M., Stewart T.A., Tamas D., Watanabe C.K.,
            Williams P., Wood W.I. and Zhang Z.
TITLE       Secreted and transmembrane polypeptides and nucleic acids encoding
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JOURNAL     Patent: WO 0073454-A 407 07-DEC-2000;
            Genentech Inc. (US)
FEATURES   source
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QY 534 GCGCGGAGCGCCCGCGCC 551
DB 61 GCGCGGAGCGCCCGCGCC 78

RESULT 14
LOCUS      AY359064
DEFINITION Homo sapiens clone DNA64884 SCGB3A1 (UNQ629) mRNA, complete cds.
ACCESSION  AY359064
VERSION     AY359064.1 GI:37183245
KEYWORDS   FLI CDNA.
SOURCE      Homo sapiens (human)
ORGANISM    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 570)
AUTHORS     Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D., Brush J.,
            Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B.,
            Dowd P., Eaton D., Foster J., Grimaldi C., Gu Q., Hays P.E.,
            Heldens S., Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S.,
            Lee J., Lewis L., Liao D., Mark M., Robbie E., Sanchez C.,
            Schoenfeld J., Seshagiri S., Simmons L., Singh J., Smith V.,
            Stinson J., Vagtes A., Vanden R., Watanabe C., Wieand D., Woods K.,
            Xie M.H., Yansura D., Yi S., Yu G., Yuan J., Zhang M., Zhang Z.,
            Goddard A., Wood W.I. and Godowski P.
TITLE       The Secreted Protein Discovery Initiative (SPDI), a large-scale
            effort to identify novel human secreted and transmembrane proteins:
            A Bioinformatics Assessment
JOURNAL     Genome Res. 13 (10), 2265-2270 (2003)
REFERENCE   2 (bases 1 to 570)
AUTHORS     Clark H.F.
TITLE       Direct Submission
JOURNAL     Submitted (01-AUG-2003) Department of Bioinformatics, Genentech,
            Inc., 1 DNA Way, South San Francisco, CA 94080, USA
FEATURES   Location/Qualifiers
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Query Match      13.9%; Score 78; DB 6; Length 570;
Best Local Similarity 100.0%; Pred. No. 0.0016;
Matches 78; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 474 GCGAGGACCGGGTATAAGAGCCTCGTGGCTTCCCGGCGAGCGCAGGTTCCCGCGC 533
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QY 534 GCGCGGAGCGCCCGCGCC 551
DB 61 GCGCGGAGCGCCCGCGCC 78

RESULT 15
LOCUS      BD082138
DEFINITION Reagents and methods useful for detecting diseases of the lung.
ACCESSION  BD082138
VERSION     BD082138.1 GI:22627748
KEYWORDS   Zea mays
SOURCE      Zea mays
ORGANISM    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
            clade; Panicoideae; Andropogoneae; Zea.
REFERENCE   1 (bases 1 to 244)
AUTHORS     Medel P.A.B., Cohen M., Colpitts T.L., Friedman P.N., Gordon J.,
            Granados E.N., Hodges S.C., Klass M.R., Kratochvil J.D., Rapp L.R.,
            Russell J.C. and Stroupe S.D.
TITLE       Reagents and methods useful for detecting diseases of the lung
JOURNAL     Patent: JP 2001522225-A 2 13-NOV-2001;
            ABBOTT LABORATORIES
COMMENT     PN JP 2001522225-A/2
            PD 13-NOV-2001
            PF 30-JAN-1998 JP 1998533078
            PR 31-JAN-1997 US 08/791710
            PI PATRICIA A BILLING MEDEL, MAURICE COHEN, TRACEY L COLPITTS, PAULA
            N FRIEDMAN,
            PI JULIAN GORDON, EDWARD N GRANADOS, STEVEN C HODGES, MICHAEL R PI
            KLASS,
            PI JON D KRATOCHVIL, LISA ROBERTS RAPP, JOHN C RUSSELL, STEPHEN D
            PI STROUPE
            PC C12N15/63, C12N5/10, C12Q1/68, C07K14/47//C07K16/30, G01N33/574 CC
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Query Match      13.9%; Score 78; DB 9; Length 570;
Best Local Similarity 100.0%; Pred. No. 0.0016;
Matches 78; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 534 GCGCGGAGCGCCCGCGCC 551
DB 61 GCGCGGAGCGCCCGCGCC 78

RESULT 15
LOCUS      BD082138
DEFINITION Reagents and methods useful for detecting diseases of the lung.
ACCESSION  BD082138
VERSION     BD082138.1 GI:22627748
KEYWORDS   Zea mays
SOURCE      Zea mays
ORGANISM    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
            clade; Panicoideae; Andropogoneae; Zea.
REFERENCE   1 (bases 1 to 244)
AUTHORS     Medel P.A.B., Cohen M., Colpitts T.L., Friedman P.N., Gordon J.,
            Granados E.N., Hodges S.C., Klass M.R., Kratochvil J.D., Rapp L.R.,
            Russell J.C. and Stroupe S.D.
TITLE       Reagents and methods useful for detecting diseases of the lung
JOURNAL     Patent: JP 2001522225-A 2 13-NOV-2001;
            ABBOTT LABORATORIES
COMMENT     PN JP 2001522225-A/2
            PD 13-NOV-2001
            PF 30-JAN-1998 JP 1998533078
            PR 31-JAN-1997 US 08/791710
            PI PATRICIA A BILLING MEDEL, MAURICE COHEN, TRACEY L COLPITTS, PAULA
            N FRIEDMAN,
            PI JULIAN GORDON, EDWARD N GRANADOS, STEVEN C HODGES, MICHAEL R PI
            KLASS,
            PI JON D KRATOCHVIL, LISA ROBERTS RAPP, JOHN C RUSSELL, STEPHEN D
            PI STROUPE
            PC C12N15/63, C12N5/10, C12Q1/68, C07K14/47//C07K16/30, G01N33/574 CC
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Qy 534 GCGAGGACCGGGTATAAGAGCCTCGTGGCCCTTGCCCGGGCAGCGCGAGGTTCCCGCGGC 551  
Db 61 GCGAGGACCGGGTATAAGAGCCTCGTGGCCCTTGCCCGGGCAGCGCGAGGTTCCCGCGGC 78

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